

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGAC  
 CCTGGTGCACCAACCAC**CATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
 GTTTTCCACCCAGCTTTTACCAAGGCCCTCCCCTGTTGTGAAGAATTCCATCAGGAAGAATCA  
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA  
 GAACCTGGCCAAAGAACTCAAGAGGCGAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAAT  
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTTGTGCTA  
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAACAGCT  
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG  
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
 CATATGACCAGAGCCAGGCCCAAGCATCTTGCTTGGTTGTACATTTCTGGTGTGATGGGT  
 GCAGTGGTGGCTCCTCTGACAAATATTAGGGGGTCCCTTCTCATCAGAGCTGCATGGTACAC  
 AGCTGGCATTTGGGAGGCCCTCCACCTGTGGCCATGTGTGCGCCCACTGAGAAAGTTTCTGA  
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG  
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTACTCAGTGGCAATGTACGGTGGATT  
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGACAAAGTAT  
 CACCAATGTATGGAGTTCAAAAATATGATCCATTAACTCGATGCTGAGTATCTACATGGAT  
 ACATTTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCCAACAGAAAGAAAT**AG**  
**AG**TGACTCAGCTTCTGGCTTCTCTGCTACATCAATATCTTGTTTAAATGGGCGAGATATGC  
 ATTTAAATAGTTTGTACAAAGCTTTCGTTGAAGTTTGAAGATAGAAACATGTCATCATA  
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTTTCTGGAGAATTAATGCGAGT  
 AATCCTCTCCCAAATAAGCACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT  
 TTGGTGAATGTGAAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTCTACTTTAAAA  
 TTTAGTAGGTTCACTGAGTAACTAAATTTAGCAAACCTGTGTTGCATATTTTTTTGGAGT  
 GCAGAAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAAGAGAGAAG  
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA  
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCATTGTTACATTCATT  
 GCTGAACCTTAACAAACTGTTTCATCTGAAACAGGCACAGGTGATGCATTCCTGCTGTTG  
 CTTCTCAGTGCTCTTTTCCAATATAGATGTGGTCATGTTGACTTTGTACAGAATGTTAATC  
 ATACAGAGAATCCTTGATGGAATATATATGTGTGTTTACTTTTGAATGTTACAAAGGAA  
 ATAACCTTTAAACTATTCTCAAGAGAAATATTCAAGCATGAAATATGTTGCTTTTCCAG  
 AATACAAACAGTATACTCATG

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**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTTCGGTGGCGCCACGTCGCGCCCGTCTCCGCTTCTGCAT  
CGCGGCTTCGGCGGCTTCACCTAGACACCTAAACAGTCGCGGAGCGCGGCCGCGTCTGAGGG  
GGTCGGACCGGGGATTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCGAAGATGTCGG  
ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCAGCGCATTTGGTTCGCGCGCCACCGTC  
GCCGTGCCCTTGGTCGGCAAACTCGGCGCTCATCAGCCGCGCCCTACCTCTTCCCTCGGCCGGA  
AGCCTTCCCTTTATCGCTTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGG  
GCTCAGGAACTGGATTCTTTTATTGGTCAATTTATTTCTATATCAGTATTCTACGCGA  
CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA  
TGTGAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA  
ACACGATTTAAGGCTGCTATTTACCTGGGTATCCTTGGATTCAACTATATCATCGGAGG  
CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTCAATGTTCA  
GATACCCAATGGACTTGGGAGGAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
CTGCCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCTGCTAGCATGAGGCGAGC  
TGCTGATCAGAATGGCGGAGGCCGAGACACAACCTGGGGCCAGGGCTTCGACTTGGAGACC  
AGTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG  
CACTTAAACACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC  
AGTACGAGACAAAGTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACCAAGTTCCAGAT  
TCTCATTCAGTCCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAAATGAC  
TACATTTTGGTGCTCTCTCTCTCCCTTTCCGCTCTGAATATGGGTTTGTAGCGGTCCT  
AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT  
TCTTGCACACATGCCCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
CCATAAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCAAAGCTGGTC  
ACAACAAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTCTTACCAATAGGGGGAG  
AAGACAGACCGGATGACGCTTCTCAGCTTTTGGAAATGCTCTGACATGACATCCGTTGTT  
AACCCTTTGCCACTCTTCAGATATTTTTTATAAAAAAAGTACCACCTGAGTTCATGAGGGCCA  
CAGATTGGTTATTAAATGAGATACGAGGTTGGTGCTGGGTGTTTGTTCCTGAGCTAAGTGA  
TCAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC  
TTTGGCTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT  
TAGGAGGATCCAGATCATGTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG  
ATTCCTCATTTCAATCTCATTTCTGGATATGTGTTCAATTGAGTAAAGGAGGAGACCCCTATA  
CGCTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTGGTTCATGTTTCAATTAATGT  
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA  
AGGGAATAACATGATTAAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAGGTTGTGTTA  
TTTTGAGTGTGAATGTACAGCTCTGTGAATCAGACAGCTTAAATACCCACACCTTTTTT  
TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAAACCAATAAAGTTTTTGAAGGCCA  
TGGCTTTTACACAGTTATTTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTCAACAGTTTTGATCAGTTTCTT  
TTCAGGAAACATTTGCTCTAACAGTATGACTATTTCTTCCCAACTCTTAAACAGTGTGAT  
GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACTCTCATTTTGAATAGAGTTTGTGTG  
TACTTCTCCATATTAATTTATATGATAAAATAGGTTGGGAGAGCTGAACCTTAACTGTCA  
TGTTTGTGTTCATCTGTGGCCACAATAAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT  
CCAATTTATGTGCAGTACCTCATTTGTACAGGCTGGAGACTCATTTGATGTATAAGAAAT  
TTTTCTGACAGTGAGTACCCGAGTCTCTGGTGTACCCCTTTACCAGTCACTGCTGCCGAG  
CAGTCATTTTCTTAAAGGTTTACAAGTATTAGAAGTTTTCAGTTCAGGGCAAAATGTTT  
ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATGACGTTTATGATTTTGTCTGGATT  
ATGTTTCTGGAATAATTTTACCAAAAGAGCTATTTGAGTTTGTGACTTGACAAGGCAAAACA  
TGACAGTGGATTCTCTTTACAAATGGAAAAAAATCTTATTTTGTATAAGGACACTCC  
TTTTGTAAACATAATCTTTTATTTGGTAAAAATGTAAATTAAGTGAACACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAAC TGGTTG  
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGT  
CCTTGTGGCCCAAAGGCTTAACCGGGGTCGCGCGGTCTGGCCTAGGGATCTTCCCCGTGGC  
CCTTTGGGGCGGGATGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATGC  
CGGGGTTCTGCGAGGGCCAGACTGGTCCATCCCATCTTGGACTTTGTGGAACAGAAATGT  
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT  
GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATGGAATT  
AATGAAGATCAATTTCAAGAAGCATGCAC TCTCCTCTTGCAAAGACCCATACATCACAGGC  
CATTTTGCACCTGTGTTGGCAGCAGAAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA  
AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT  
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
GAGGGAAGTCTTAGAAAATCAAAGAGGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
AATAATTTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAATGCATTT  
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCTCCCTCC  
CACAAAAGGCTGAAGATTCTGGCTTAGAGCATCGGAGCATTGAAGGACCAATAGCAAC  
TTATCAGTACTTGAACAGAGAAC TTCGGCAACGAGAACCATATCTCAAGCAGAAGAGAGA  
TAAGTTGATGTCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
GAAAACCCATGGGGAGGTAGAGGAATGACAGAGAAACAGAAATGACAGCAGAGGAGAAAG  
CAAACTACTTAAGAGAGGATGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA  
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATGTCTTAAAAATAAATTATTTAGTC  
CTTACACTG

**FIGURE 6**

MAAEEDDEVEVWVESIAGFLRGFDWSIPILDVFEQKCEVNCKGGHVITPGSPPEPILVACVP  
LVFDDDEESKLTYTEIHQEYKELVEKLLGEYKLEIGINEDQFQEACTSPLAKTHTSQAIIQ  
VLAEDFTIFKAMMVQKNIEMQLQAIRI IQERNGLVPCLTGSDVVSLEHEEMKILREVL  
RKSKEEYDQEERKRKKQLSEAKTEEPTVHSSAEAIMNNSQGDGEFAHPPESEVMKHFANQS  
IEPLGRKVERSETSSLPQGLKIPGLEHASIEGIANLSVLGTTELRLQREHLLKQKFRDKLMS  
MRKDMRTKOIONMEOKGKPTGEVEEMTEKPEMTAEOKSLTLKRLRLAEKLEKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGCGGCTTAGAGGGAGGGGCTTTTTGCCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTCTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAC  
 AGTGGGAATGGAAAAACAGTGCCTGTAGTCATCCTGTAATATGCTCCTGTGCAACAATGTATAC  
 ATTCTCTGCTAGGTGCCATATTATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCTCGGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTCGCCT  
 TTCTTTATTTCTGGATAAATTGATTGCTTCTATGCTCTGCTCATCTTCAACCAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAA  
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTGCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCAGATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAAGAAGTGAGTGTCCCAGAAAGACAAATTG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTCAGTC  
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGGTTTTATTCTTCAATGGCT  
 AATATCTATAATGAAGAAGTACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA  
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTTTAATGGGCTGACTCTGGGCCCTTCAGAGGA  
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTGAATTCGATTCCAGGGGCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA  
 CATGTTCCATGCTCTTGATGGCCAGGTTACCAGTGTCAATATCACACAGTGTCTGTCCCTGG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAAGCCCCATCAGTCTCTTCTCTATA  
 TTTATTTATAATGCCAGCAAGCTCAAGTTCCGGAATACGCCACCTAGCCAAAGAAAGCTCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
 CCAAAACCCAAAGATGATGAGTCAGATGAAGATACTTTCTAACTGGTACCACATAGTTTGCA  
 GCTCTCTTGAACCTTATTTTTCACATTTTCAGTGTGTTGTAATATTTATCTTTTCACCTTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATTCTTGCATATATCTAGTCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTTAAAGAAGTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCCTTCAAGCTTCCAAAAAATCTGTAATAATCATGTGTAGCTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTGATTTCATGTTTCAAGT  
 CTCTCCCTTTTTAACATTTATAAAGCTAGGTTGTCTCTTGAATTTTGGGGCCCTAGAGATAGT  
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTGTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGAAATTGGATTTTTGT  
 AATAATCTTTTGATGTTTTAAACATTGGTCCCTAGTCACCATAGTTACCAGTTGTATTTTA  
 AGTCATTTAAACAAGCCAGGTTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
 GTCAATCTCTGAAATATTACATTTTGGAGAATAAGAGGGCACTTTTATTTTATTAGTTACT  
 AATTCAAGCTGTGCATTGTATATCTTTCCAAGGTTGAAATGCTGGCTCAGATCATAC  
 CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT  
 AGCAAAACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA  
 AAATTAGCAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGG  
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACTGTAACCTTATGACCTTATGTGTG  
 CATCTCAGAACTTATACATTTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
 AGGTAATATACTATTATATAATTCATTGTGCTTCCCAATAATATGACTGGCAAGAAATG  
 GTGGAATTTGTAATTAATAATATTAAACCT



**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV  
IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESDETF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

**FIGURE 10**

CGTGCCGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATACATTCCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTCATGAAGTGGTCCATTCCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATT CAGGATAGTGTCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGCTAGCGCGCGCGGGC  
TGGTCTAAGGCTGCTACGAGCGAGCTTGGGAGGAGCAGCGCGCTCGGGGACGAGGAGCAT  
CCGCTCTACAGGTCCCAAGCGCGCTGGCCGCGGGTCACTGCCCAAAGGAGAGCGCCGAG  
AGCGGCTCCGCGCGGGGCTGCTACCCACAGACTCCTCCAAGACTGAAACGCCGCGGCCA  
GGTGAAGAAAGAACGAAAAAGAAAGAAACAGTTGTCTGTTTGCACAAAGCTTTGCTATG  
CACTTGGGGGAGCCCCACAGGTGACGGCTGTGCCCTGGGTTTCTTCCTCAGATCTAG  
CTATTGGATGGCTGAGTCAAGTGGGCCCTTTTCTCTGCCTCCATCACTCTGTTGTGGGCGGAG  
CTGGGATGCCATCAGACACCCCTGGTGGGCTCTGCATCAGAAATCCCCTGGACCTGCC  
TGGGTGCGCTTATGCCCTGGATCATCTTCTCCAGCGCCCTGGCCGTATTGCCTACTTCC  
ATCTGCTGTGCTGGCGCACTCCCAACGCGGACAGCTATTGGTACTGCTTTTCTATTGGCT  
CTTTGAAACAATGGTCAAGTGTTCCTATGTTCCTACTCGGCTCTACCATGTTCACTCAGCA  
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCCGATGACTGTGGAAGTGTGGGCA  
AGTCTGGGACCGCGCATCCAGGGACAATCTGGGCGCAAGCAGACAGCTTGTTCACAG  
ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACTACATACATGGCACCACTTCACAC  
AGGGAACCGCAAAAGGCATACCTGCTGGCAGCGGGGTCACTGTCTGATCTATATAAATCTG  
TGCTGTCACTCTGATCCTGGGCTGCGGGAGCAGAGAACCCTATAAGCCGACAGCTGTG  
AGCCAATCGCCTACTTCCGGGGCTTACGGCTGGTCATGAGCCACGGCCCATACATCAA  
ATTACTAGCTTCTCTTCACTCTCTGGCTTTCATGCTGGTGGAGGGAACTTGTCTTGT  
TTGCACTTGCATCTTGGCTTCGCGAATGAATCCAGAATCTACTCTGGCCATAGCTCT  
CGGCCACTTTAACCATTTCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAGACAGCT  
GTATATTTTGGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCTCATGAGAGCTAA  
CCTCATATTACATACATCGGTGAGTCTGGCAGCTGGCATGAGTGGCAGCTGCCCTCTTAC  
TACCCTGGTCTCATGCTGCTGATGTCTATTGACACTTCCATCTGAAGCAGCGCCCATTCAT  
GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTCAACAAGTTGCTCTGGAGTGT  
ACTGGGCATTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCGGTGGCTGCTCGAGC  
CGGAACGCTGCAAGTTTCACTGAGCAATCATGCTGTCGACATGGCTCCCATAGTTCTCATCTG  
CTGGGCTGCTGCTTCTTCAAATGTACCCATGTGATGAGGAGAGGCGCGCGCAGAAATAAGAA  
GGCCCTCTAGCGCACTGAGGGACGAGGCGCAGCACTCTGGCTCTCGAAGAACAGACTCCACAG  
AGCTGGCTAGCATCTCTCTAGGCGCCGCGACGTTGCCCGAAGCCACCTGCAAGAGGCCACAG  
AAGGATCAGGACCTGTCTCGCGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
CTGAAGACTCAAGGAGGTGGCCCGAGACACTTGTGTGCTCACTGTGGGCGCGGCTGCTCTG  
TGCCCTCTCGGCTCCCTTCTGCTGCTGTGGGGCCAGCCCTGGGCTGCCACTGTGAATA  
TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAGACTTTTTTTTACAGAGCC  
TAATTAATAACTTAATGACTGTGATGATGACGAATGTGTGTATGTATGTCTGTGAGCTA  
TTAATGTTAATTAATTTTATAAAGCTGGAAGG

**FIGURE 12**

MWLRWALS LPPSSCLWAEFGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSH TARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAV  
IILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGT EPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

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**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGT  
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

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**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT  
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
 CAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG  
 ACTTTCATTTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG  
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
 AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTCGACAGTGGCAATTTGGGACTG  
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA  
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG  
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT  
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA  
 TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
 TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYD  
TAPCPINNERTRLISRDI

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**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGGTTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA  
CGTTCCTGTTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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**FIGURE 17**

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG  
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCGGGTGAC  
 CTTGCGCTTGTAATTGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
 AGGCTGGAGGAGGTGCTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA  
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT  
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC  
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT  
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT  
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT  
 CCCATCGTGAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCTCTGTGT  
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG  
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCTCATTAAAAAATTT  
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA  
 CACATTGATCTGGATTTTCTGTTTGCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA  
 TGTGGTCTCTAAAGCCCTCATGTGTTTTGATTGCTTCTATAGGTGATGTGGACACTGTG  
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAAATGCTGTTTGT  
 GGCCGGGCGCGGTGGCTCACGCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGTGATTCT  
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT  
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC  
 AGGAGAAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCCTGCACT  
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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## **FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLLPRGRRIGSTEEAGGRSLWFPSDLAELRESEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLGALFGPWLGLLCCVLTSVGATCCYLLSS  
IFGKQLVVSYFDPKVALLRQKVEENRNSLFFFLFLRLFPMPNWFNLNLSAPILNIPVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domains:**

amino acids 101-123, 189-211

#### **N-glycosylation sites.**

amino acids 172-176, 250-254

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

#### **N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

#### **Amidation site.**

amino acids 27-31

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

#### **Protein splicing proteins.**

amino acids 25-31

#### **Sugar transport proteins.**

amino acids 162-172

**FIGURE 19**

CCGAGCGGGAGGAGCCCGAGGGGCGCGAGCCCGCATGAATCATTGTAGTCAATCATTTT  
 CCAGTTCTCAGCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACAGCTCAGAA  
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA  
 TTTATGACAACTTTAGAGACTGTTGATTGGTGAGACAGACCGCCATCAGTGTGGCATG  
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAGAATGAACCTCAGAGACC  
 CCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
 TGCTCACTGCCTACTTTGTGATTCAACCTTTAGCCCATAGCACCTGAGCCAGTGCCTTCT  
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGTGATGAAGACAGACCTTTC  
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCATTCTGCC  
 AACTGCACTGGCTGTGCCAGAAACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA  
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC  
 AGCATTTTTTGTGCCAGTACCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
 TGGTGGCGCTGCTTCTGAGCGGTGGTTCCTTATCCATGGAGGAGACCTCTGAA  
 CAGATCACAATGTTACGTGAGCTTTTCTGTTTCACTCACCTGCCATTTCAAAAGATG  
 CCTCTTTAAACAAGTGCTCCTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
 ATGCCGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCTCCCTTCCA  
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTG  
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
 GGAACCGCTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA  
 AAACAGGTTGAAAGGGGAAAAATAAAAAACAAACGATGAAACTGCAAAA

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**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEFIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFVP  
FTHLPFPKDasLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP  
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

CCACGGTGTCCGTTCTTCGCCCGGGCGGACAGTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC  
AAGGGACAGTGGTTTCCGAAC TGCCAGCTCAGAAATAGAAAATAACTTGGGATTTATATT  
GGAAGACATGGATCTTGTCTGCCAACGAGATCAGCATTTATGACAAACTTTT CAGAGACTGTTG  
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGT CAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAATGAAC TCAGAGACCCCCCGCAGTATCTCTCCTTATAGT  
TGTGTATAAGGTTTCGCAACCTTGGGATTAATCTTGCTCATCTGCCTACTTTGTGATTCAAC  
CTTTTCAGCCCATAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

**FIGURE 22**

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG  
 CCACTGTGCGCACCTGCTAGACCGTGCTATGAGCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCTTGCACCCACCAATGGCAGCCCCACCTCTTTGAAGACTTCCAGGCTTTTGTGGCA  
 CCCCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACTGATGCCAGTTTGGAAATG  
 GACACGTTATGCTAAGAGCCAGCACCTTATGTGAGTTTCTGGAATGCGCTGCTATGCATGTCT  
 TATGAGCAGTGGGACAGCGCGCAGTGGGAGCGCGCCAGAGTCTGCTGGCGCTCTCCAGGAGC  
 TGGTGTCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGTCTG  
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT  
 CGCGAGCCCTGTGGGGCTGGCGCTGAGGGACACTCCCATCCCCCGCTGGAAACTGTCCA  
 GCGCCAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC  
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTTGACACCCACCGAGGAGGC  
 CTCACTGCCTCTGGCAGTGACCAAGAGGGCAAGTGAGCACCCACCAGGTTGCTCGAGG  
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGACGACGAACCTG  
 GATGAGCAGCGTGAGAAGCTGGTGTCTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT  
 GGTCCCAGGGCTGTCTGGAGGTACCCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC  
 CGGTGGAAACCGAGGAGGCGATCGGCTATGATTTCCGCGGCCACTGGCCCGAGCTGGGTGAG  
 GTCCACTGCGGCTTTCAACCTGCGCCGTTGAGCACTTGAGCTCTTCTTATCGATCAGGC  
 CAACTACTTCTCACTTCCATGCAAGGTGGGACGACCCAGCTCTCATCTCTAGCCAGA  
 CTCGCGAACCCAGCTGCGCCCATCCCAACCCATACCCAGGTACGGAACCAAGGTGTACTG  
 TGCTCTCTGCGCCTACGGCCCTCTCAAGGCTTACCTAAGCAGCGCTCCCCCAGGAGCTG  
 GCTGCGTGCTCTCAGGCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT  
 TGATGCACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTGTC  
 CCTGGGTCTCTCAGGACTACGTGTCCCCAACCTTGGAACCTCAGCAACCCAGGCGCTGTCCG  
 GGACTCTCTAAGCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT  
 ATGAAAGCTTTGAGAGCCAGCAGGACCATTGACAAGTTCCACTATGGCACCCCACTACTCC  
 AATGACGACGCGGTGATGCACCTACCTACCTGCGGTGGAGCCCTTCACTCCCTGCAGCTCCA  
 GCTGCAAAAGTGGCGCTTTGACTGCTCCGACCGGAGTTCCACTCGGTGGCGGAGCTGGC  
 AGGCACGCTGGAGAGCCTGCCGATGTGAAGGAGCTATCCCGGAATCTTCTACTTTCCT  
 GACTTCTGGAGAACCAGAACCGTTTTGACTGGGCTGTCTCCAGCTGACCAACGAGAAGGT  
 AGGCGATGTGGTGCTACCCCCGTGGGCGGAGCTCTCCTGAGGACTCATCCAGCAGACCCGC  
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC  
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCAATTA  
 TCAGCAACTTTGGGCGAGCTCCCTGTCAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA  
 GCTGGAGGAAGCAGCCATCGCCTTGACGCGCTGGACACTAATCACTAGCATCTTCCAGCA  
 CTTGGACCAACTCAAGGCATCTTCGACAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCCAGCTGGTTGCCCTTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAAGCCCC  
 ACCATGGGCGAGCCACAAAGCAGCAGCGACTGCTGAGTGGCCGCTGGTGCCAGGCAAGTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTACGCGGTGGCCACTGGG  
 ATGGCAGCTGTGGGTGCTGCACTACCCCGTGGCAAGCTGTTGAGCGCTGAGCCTGCACT  
 CTTGATGTAGTAACTTGCTTGCACCTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG  
 GGACACCACTGTCATGGTGTGGCGGCTCTGTCATCAGGCTGGTCTGTGCTAGTGGCCTGGCAG  
 CAAAGCCTGTGCAGGCTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACCTGACATGCTGTGTCTGAGTCTGAGGATGGAACCTGTGATCATACACACTGTACGCGC  
 CGGACAGTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCTCTGGACCTATTTTCCACC  
 TGGCATTGGGTCGGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAGCGCTCGGGGCC  
 CAGGTCACTTCTCTTGCACTGTATTCTAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT  
 GGCAGAGCAGCTTACAGCCCTGACCGGTGACAGGAGCTTTGTGTTGCTGGGACGCGCCAGT  
 CGCCCTTGCACTCTTCAACTAAACACACTGCTCCGCGCGCGCTCCCTTGCCCATGAAG  
 GTGGCCATCCGACGCGTGGCCGTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCTGGAGGA  
 TGGCAAGCTCATCTGTTGGTGTGCGGGGACGCCCTCTGAGGTGCGGACGAGCCAGTTTCGCGC  
 GGAAGCTGTGGCGGCTGTGCGGCGCATCTCCAGGTGCTCTCGGGAGAGAGCGGAATAACAAC  
 CCTACTGAGGCGCGCTGCACTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCGAGGCGCTG  
 CCGCGGAGGCGCCCGCCAGAAGTCTGGCGGGAACACCCGGGTTGGGACGCCAGGGGCTGA  
 GCGGGGCCCACTGCGCCAGCTCAGGAGTTGGCGGGCGATGTTACCCCTCAGGGATTGGCGG  
 GCGCGAAGTCCCGCCCTCGCGCGGTGAGGGGCGCCCTGAGGCGAGCACTGGCGCTCT

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**FIGURE 23**

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPPELLQEDQLGEDELAEELETP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVPFWVLQDYVSPDLDSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKELIP  
 EFFYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPPWASSPEDFIQQRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEALNVFYCYTEGAVDLDHVTDERERKALEGII SNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPMTGSHKTRQLLSPGVPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIIYLISGRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAS  
 CVAISTELDMAVSGSEDTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA  
 WERPGAQVTVTSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTEAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

**CGG**ACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
 CACGGCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCAT  
 CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC  
 TGGACCCCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT  
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCCTTGTGCAG  
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC  
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAATAATTTATCAAGTTC  
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCTGCTGGACAAAGTACAGA  
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTTT  
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC  
 TGGTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTACGCGT  
 TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG  
 GCTCCTTGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
 GAGGCGCCCCCGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC  
 ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
 AAAAAAAGTTTTAGGCCAGGCGCGTGGCTCAGCCTGTAATCCAACACTTTGAGAGGCTG  
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC  
 TCGGAGGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA  
 AAAGATTTTATTAAGATATTTTGTTAAGTCA

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**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLF  
WTLNWWLALGQCVLGAFASFYWAFHKPDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRI PGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMKSLLKILGKKK  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTGACCGCCGCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGCGT  
 GGCT**TATG**TCGTGTCGGAATTTCCGCAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT  
 CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG  
 ACCATTGGATAATTCTTCAACCTGATGAAGACACTATATCTTTGTGTGTGACTCCCATAGG  
 CCAGTCAATGTCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGA  
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCGAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT  
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGCTCTGACGCG  
 CCACGTTTCCCGCCACACCAACCGGAACGAGGATGAGGAGAACACACATCTCCGTGGACTGCA  
 CAGCATATCTCCTTTGAGTATGACCTCCGCGCTGGTGCTCTACCAAGCACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGCTGCAAATAAA  
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGSATGGCT  
 CAGGGACAGATCACTTATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATTGGCTTGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC  
 CTTTGACCAACCTCGTCATCTFCCAGGGGCGCTTTCCTGTACTGCTCTCTCATGGAGGGCAC  
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCCTTTGTGTGTTGCACAAAGAACCGCGCTGCAAATGCTGCCCTGGTGATGGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTG  
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAGCACCAGCTCCCGGA  
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACTATTATTTCCCTGCTGTCC**TAGA**AAATTGATTCTTCAGAATGACCTTCTTATT  
 TATGTAACCTGGCTTTCATTAGATTAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
 TTTTATAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAYEDI FRDEEEDDEHSGNDS DGSEPSEKTRLEEEIIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLRH  
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR  
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMI EESANKFGMKDMRVQTF SIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLPLVMAAP  
LSMEHGTVTTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DLSVIELKAEDRSKFL  
DALISLLS

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**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCGGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

CGGCTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTTTCGTGGCCTCGGANGTGGAT

**FIGURE 29**

CAGGAACCCCTCTCTTTGGGCTCTGGATTGGGACCCCTTTCAGTACCAATTTTTCTAGTGAAC  
 CACGAAGGGGACGATACCAGAAAAACCCCTCAACCCCAAGGAAATAGACTACAGCCCCAATTG  
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAAGAGACAGTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAAAT  
 GAGTAAAGTACGCTCCGGTCAACA**TGGT**GACAGCGCCCTGGGTCCCGCTGGGCAGCGCTC  
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTGCCAACGGTCTGTGACTCTGAGGACCCCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCTCCGGCCGCCACGCCCTGCCTGAGATCAGACCTACATTAATATCACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCCTGCCAGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG  
 GCGCCCGCTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GGCAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCGACCGCCAGTTTGTCTGCCCTGCTGGCATCTACTTCTCAGCCTCAATGTGC  
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAAGAGGCTGTATC  
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCAGAGAAGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACTCATCAAGGCCGAGGACGACT**GAGGG**  
 CCTCTGGGCCACCCTCCGGCTGGAGAGCTCAGGTGCTGGTCCCTGCCCTCAGGGGCTCAG  
 TTGTGACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCGGGGACCTGGCATCTTGGGGAGA  
 CCGTGCTTATCTTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCT  
 TGGAGCTTTTTAAGAAGCTTGTCAACCTAAATATCTAGAAGCTTTCCAGCCTCGTAGGCC  
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACC CGGGGTTCGTGTTAAATGCAGATTCT  
 GACTCAGCAGCTGTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTCTCTGGGTGATGCTG  
 ATGGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATTTCTAG  
 TACTTTCTGAACATTCTGGAATCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTCT  
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGAATCTCAGTTCTACTGC  
 AACCTCTGCCCTCCCGGTTCAAGCGATTCTTCTGCCCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCGCTGCTACCATGCTTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCTGCCCTCAAAAT  
 GCTGGGATTCAGAGTGTGAGGCCACCGTGCTGGCCCAATTCCAACATTCTTAAATTTCTCAT  
 CCTCTCAGGGCTCCCGTGTGCTATGTTCTCTTACCCTTCCCTCTCTCTTCTGCTCAGGCC  
 TGACCACTGCAGCCACCGTTTCAATTTATTCATTATTAACACTGAGCACTCAGTCTGTGCT  
 GGGTCCCGGGGAAGGTTGAGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTACTGGCCA  
 TGACAGCCAGCCAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGGCTCTGGGG  
 GCTGTGTTCTGGGTGTTTCAAGTGCTGCTGGTCTCTCCATTACCCACTGCTGCCCAAGGCTGG  
 TGGGACGGGTTCCCGGTGGCAGGGGAGGTATCTCCTTCCGCTCTCTCATCCAGCTGCCCA  
 TGCTCATCGTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCAGGAGTGTGGGGGCTATTGGGGGGTGAAGTGGCCCCCAAGAAATGGAACCCACACCA  
 TAGCTCTCCCAACAGCTGATACGGCATCTGCGAGAAAGACTTCCCTCTCTCAGTGGGATCCC  
 CTTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAGTCACT  
 GAACCTCCGTTTCCCAAGGGCTCCAGCTGCCCTGCCCTCAGCACTGATGTCTGTCCCAAGTGCT  
 CTCTGCCCTCATGCCCCCTCTCACC GGCCAGTGCCCGCACTCTCAGGCTTTATCAAGGT  
 CTAAGGCCCCGGTGGGCGACTCTCTGCTCAGAGCCCTCTCCGGCTGGTGCTGCTCTTAC  
 AAACAGCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGGCTCAGCAGGTCTGGGG  
 AGCTTAGACAAGAGGGACCTCAGGCTTCCGTTTCTTCTCCAGGTTGGGGTGGCTGGT  
 GTTCCCCTAGCTTCCAACCCAGGTGGCCTGCCCTTCTCCCAAGAGGGGAGGGCGGCTCCGC  
 CCTTGGTGCTCATCGAGACTCTGGGGCTGAGGTGCCCGGGGGTGATCTCTGGTGCTAC  
 AGCCGAGGGGAGCGGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCCAGGA  
 AGACTGTGCTATAAACACCCTGCCGTGATCCTGCCCTGCCTGACCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGAAATGCTGTCTCCTCTTGAAAAA

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## FIGURE 30

MVTAAALGPVWAAALLLLLMCEIRMVLTDFDRAVASGCQRCCDSEDFLDPAHVSSASSSSGRPH  
 ALPEIRPYINITLLKGDKGDPGPMGLPGYMGREGPQGEFPGPGSGKDKGEMSGAPACQKRF  
 FAFSVGRKTALHSGEDFQTLLFERVFNVLGCGFDMATGQFAAPLRGIYFFSLNVHSHWNYKET  
 VYVIMHNQKEAVILYAQPSERSIMQSQVMGLDLAYGDRVWVRLFKRQRENATYSNDFDTYIT  
 FSGHLKAEDD

### Important features:

**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGCTGCCCGGCCGGCTCCCTGCGCCGCCCGGCTCCCGGGACAGAAAGATGTG  
 CTCACGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG  
 GCTGCCCCATCGGGTGCAGTGCAGCGACGCCACAGACAGTCTTCTGCAGCTGCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGCTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCTGCCGGGCTGACGCTCCTGGACCTGTCTAC  
 AGAACAGATGCCAGCCTGCCAGCGGGGTCTTCCAGCCAATCGCCAACTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCGCGCCT  
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC  
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGCTGCGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT  
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTACGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACAC  
 CGCATTTGCCAGCTGCGGCGCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATG  
 TCGACAACCTTAAGCTGCGAGCCCTGCTGCGGACCTCTCGGGCCTCTTCCCCGCGCTGCGG  
 TGTGTCGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTCTGCTGCTTTGGCCCTG  
 GGTGCGCGAGAGCCACGTCACTGCGCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCA  
 AGAACGCTGGCCGGTGTCTCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCAC  
 ACCACAGCCACAGTGCCACCACGAGGCGCTGGTGGGGAGCCGACAGCCCTTGTCTTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCACAGCCCGCTTCCA  
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCATGCCACCTGGGGACACGGCACCTGGCGTGTGTGTGCCCGAAGGCTT  
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA  
 CGCCGAGGCCACACGCTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACTTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCCTTGGGG  
 CCCGGCGGGTGCCGAGGGCGAGGAGGCTGCGGGGAGGCCCATACACCCAGCCGCTCCA  
 CTCCAACACGCCCCAGTCAACAGGCCCGGAGGGCAACCTCGGCTCCTCATTGGCCCG  
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG  
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC  
 GGAAGTGGAGGAGTGAAGTCCCTTGGAGCCAGGCCGGAAGGCAACAGAGGGCGGTGAG  
 AGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTCGGCCTC  
 CAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCG  
 GGCTCTCAGCGAGTGAGATGGCCAGCCCCCTCTGCTGCCACACACAGTAAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGCAGACAGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA  
 CCTCGGTCTCCTCATGTGTGATGCTGTGGCCAGCTGACAGCCCTCAACGTCCTCCAGAAC  
 CGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCTGGGGGCCAGTGAAGGAAGTCCCGGAAGAGCAGAGGGGAGAGCGGTTAGCGCGCTGTG  
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATATTATAGAGATCCTTTCCCATTTATTCTG  
 GGAAGATGTTTTTCAACTCAGAGACAGGACTTTGGTTTTTGAAGACAAACGATGATATG  
 AAGGCCCTTTGTGAAGAAAAATAAAGATGAAGTGTGAA

MCSRVP LLL L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F E N  
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R  
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P  
G I L D T A N V E A L R A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G  
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G  
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S  
S S L A P T W L S P T A P A T E A P S P P S T A P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R R H L A C L C P E  
G F T G L Y C E S Q M G Q T R P S P T P T P P P R S L T L G I E P V S P T S R V L G L Q R Y L Q G S S V L C R S R L R  
T Y R N L S G P D K R L T L R L P A S L A E Y T V T Q L R F N A T Y S V C M P L G P G R V P E G E A C G A E H T P P A  
V H N S H A P T Q A R E G N L P L L I A P A L A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G  
P L E L E G V K V P L E P G K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I



**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTCATCATCTCATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAACATGAGACTCATCAG  
 AAACATTTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGAACCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGG  
 ACCCCAGGCAACAGCAGACTGGATTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAGA  
 TTTTTCATTCTGTCTCCAACCTGAGAGTTTGTATTCTATGCCATAACAGAAATCAACAGCTGG  
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGAGCT  
 AAGAGTGTAACTTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT  
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA  
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATCTGTCT  
 TTCTTTAGGATTCAGAACTCTTCTCTCATTATGAAGAAGGTAGCTGCCCATCTTAAACACAAC  
 AAACTGCACATTGTTTTACCAATGGACAAAATTTCTGGGTCTTTTGCCTGATGGAATCA  
 AGACTTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA  
 ATGCAACGAAATCTTAGTTTGA AAAATGCTAAGACATCGGTTCTATTTGCTTAATAAAGTTGA  
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTTGGCATACATCAGTGGAAACACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
 TCAAAATCTGTAATGAGAACTATAAAATGGAGCATGTACATTTTCAGAGTGTTTTTACATTCA  
 ACAGGATAAAATCTATTTGCTTTTGGACAAAATGGACATAGAAAACCTGCACAAATCAAAAT  
 CACAAATGCCACACATGTTTTCCCGAATTATCCTACGAAATTCGAATTTTAAATTTTGGC  
 AATTAATATCTTAAACAGACGAGTTGTTTAAAGAAGCTTCCAACCTGCTCTACTTTGAAAACCT  
 CATTTTGAATGGCAATAAAGCTGGAGACACTTCTTTAGTAAGTTGCTTTGCTTAACACACAC  
 CTTTGGAAACCTTTGATCTGTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA  
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCTATCAATAAATTTGCTGATCTGTCTTCAG  
 GTGCTTGCCCAAAAGTATCTCAAAATCTTGACCTAAATATAACCAAAATCCAAATCTGTACCTTA  
 AAGAGACTATTCATCTGATGGGCTTACGAGAAGCTTAAATTTGCATTTTAAATTTTCAACTGAT  
 CTCCTCGGATCGAGTCATTTTCAGTAGACTTTCAGTTCTGGAACATTTGAAATGAACTCTATCT  
 CAGCCCATCTCTGGATTTTGGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATCGGGGAAGAA  
 ATCCATTCGGGTGTACCTGTGAATTA AAAATTTTCATTCAGTCTGAAACATATTCAGAGGCT  
 ATGATGGTTGGATGGTCAGAGTTCATACACCTGTGAATACCTTTTAAACCTAAGGGGAACATAG  
 GTTAAAAGACGTTTCTCTCCACGAATTTATCTTGCAACACAGCTCTGTGTGATTTGCACCATGT  
 TGGTTATTATGCTAGTTCTGGGGTGGCTGTGGCTTCTGCTGCTTCCACTTTGATCTGGCC  
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCAAGGGTTAGGAAAACAAACCA  
 AGAACAACTCAAGAGAAATGTCCGATTCACGCAATTTATTTTCATACAGTGAACATGATTTCTC  
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGTTTCTATCTTGATTTGC  
 CTTTATGAAGACTACTTTGACCTGGCAAAAGCATTTAGTGA AAAATTTGTAAGCTTCTTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGCCTAT  
 ATGAATTTCTACTTTGCCCAACCAATCTCTTCCATGAAAATTTCTGATCATATAAATTTCTATC  
 TTAATGGAACCCATTCCATTTCTATTTGCATTTCCCAAGGTATCATAAATGAAAGCTCTCTCT  
 GGA AAAAAGCATACTTGGAAATGGCCCAAGGATAGGCCATAATGTGGGCTTTCTTGGGCCAA  
 ACCTTCGAGCTGCTATTAATGTAAATGTATTTAGCCACAGAGAAATGTATGAACTGCAGACA  
 TTACAGAGATTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTATGAGAACAGATTGTCT  
 ATAAATCCCAAGCTCCTTGGGAAGTTGGGGACCATACATCTGTTGGGTGTACATTTGATTA  
 CACCTTTATGATGGCAATTTGACAAATTTTATTA AAAATTA AAAATTTGATTTTCCCTCATATA  
 TCAGTTTCTAGAGGATTTCTAAGAAATGTATCTCTATAGAAACACCTTTCACAAAGTTTATAAGG  
 GCTTTATGGA AAAAGGTGTTCTGATCCAGGATTTGTTATAATCATGAAAATTTGTGGCCAGCTGC  
 AGTGGCTCACTCTGTAATCCCAAGCACTATGGGAGGCCAAGGTGGGTGAGCCACGAGGTCAA  
 GAGTGGAGAGCACTCTGCCAACATGGTGAACCTGTCTCTACTAAAAATACAAAATTA  
 CTTGAGCCGGGAGGTGGCAGTTGCACTGAGTGGAGTGGAGCCAGCTGCATCTCCAGCTGGT  
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGGA AAAACATCC  
 TCATGGCCCAAAAATGAAGGTCTAATTCATAAAATATAGTACATTAATGTAATATAATATTA  
 CATGCCACTAAAAAGAAATAGAGTAGCTGTATTTTCTGGTATGGA AAAACATATAATAT  
 GTTATAAATCTTAGTGTGGTGCAAAACATTTTGGGTTTTTGGCATTGAAATGGCATTTGAA  
 ATAAAGGTGAAGAAATCTATACAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTTGA  
 TTACAGGAGCAATTTGATTTCTATGTTGTGTTATTCATAATGTGTAATTTGAATTTTGAAGATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTCAGGCT

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**FIGURE 34**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ  
LQSSDFHSVSKLRVLILCHNRIQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTPMICEEAGNMHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLTAKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP  
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENCSPETVVNMNLSYNKLS  
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHF SRLSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNFPRCTCELKNFIQLETYSEVMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV  
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNLFHENS DHIILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM  
RTDCL

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[illegible]

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPLP  
AGPGEEWERRPQEP RP PKRATKPKKAPKREKSAPEPPP GKHSNKKVMRTKSEKAANDHS  
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTVWTVKNGSGDMI  
EGNSEKEIPVLNELPVMVARYIRINPQSWFDNGSICMRMEILGCLPLDPNNYYHRRNEMTT  
TDDLDFKHNNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG  
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPWFLSENATVAA  
ETRAVIAMWEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTEHTPTPDHVFRLWLA SYAST  
HRLMTDARRRVCTEDFQKEEGTVNGASWHTVAGSLNDFSYLTHCNFELSIYVGC DKYPHES  
QLPEEWNENRESLIVFMEQVHRGIKGLVRDSHGKGINAIISVTEGNHDSITDGDYWRLL  
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPAR  
LKL RGRKRRORG

**FIGURE 37**

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTTCTCTAGCCCTTCTGTCTCTCTTGGCCAAGCTGCAGGGG  
 ATTTGGGGGATGTGGGACCTCCAAATCCAGCCCGGCTCAGCTCTTCCAGGTGTTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCCAAGTTGT  
 TTCCAATTTCCAGGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTCTCCCTGCCAGACACCACTTTTC  
 CCGTGGACAGAGTGGAAACGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAAGTTGAGAAAGAACTTTTAA  
 GTGAGGGAATATGCTCAATTAATTAGTGTGTATGAAAAAACTGTAAACCTAACGTGTCGGAATTGACATCAT  
 GGAGAAAGATACCACTTTCTACACTGACTGGACTTCAGCTGATCAAGGTGAAGTGAAGGAGATGGAAAAAC  
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATGTTGACACAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTGGTAGACAAGCTTGAGACACTAGACAAAAACAATGCTCTGCCATTGCCGAGAAATCGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAAGATCAAACACCCCTGTGCTCCACCTCTCTCCACTC  
 CAGGAGCTGTGGTCTGATGTTGGTGGTGAACATCAGCAAACCCCTGTGGTTCAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCGAGCTTCAAACAAAGCACTGTATGGGTGGCGCC  
 ATTGAAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACACCACTGGATGATTTGCTATTGTATATA  
 ATGCTCGAGAGTTGGGATCACCTATGGCCAGGTAGTGGTACAGCAGTTTACACACACACATGTACGTCAAC  
 GTGTACAAACCGGGAATATTGCCAGAGTTAACTGACCACCAACAGGATTGCTGTGACTCAACTCTCCCTAA  
 TGCTGCCATATAAACCCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTGTGGGTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCCCTCATGGTATGTGGGGTTCT  
 GTATGCCACCCGTACTATGAACACCAAGAACAGAGAGATTTTACTATTATGACACAAACACAGGGAAGAGG  
 GCAAACTAGACATTGTAATGCATAAGATGCAAGAAAAAGTGACAGAGCATTAACTATAACCCCTTTGACCAAGAA  
 CTTTATGCTATAACGATGTTTACCTTCTGAATATTGATCTTTCTGTCTTGAGAGGCCCCAGTAAGAGCTGTTTA  
 GGAGTTAGGGGTGAAAGAGAAAAATGTTTGTGAAAAAATAGTCTCTCCACTTACTTAGATATCTGCAGGGGTGT  
 CTAAAGTGTGTTCATTTTGCAGCAATGTTTAGGTGCTAGTTCTACCACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTCTTGGAATCATCTGCCTCTTCAGGCGCATTTCGAAATGAAGTCTGTCTAGGGGTGGGA  
 TTGTGAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCATAGAGGCTTTAAATTA  
 GGAATTAAGGAACTTAAACCTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAATATTGCCCAATGACTAGTC  
 CTCATTCATAGTACCCCTAATTTCTCCATGCCGGAAGAAACCTGGGAGCTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGGACCAATCTCCAACCTTTTTTCCCTCACTAGCACTGGAATGATGCTTTGTATGTGG  
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGGCCCTTTT  
 ATGCATTAAATTGTACATGGCAATAAATCCGGAAGGATCTGTAGATGAGGCACTGCTTTTCTTTCTCTC  
 ATTTGCCACTTACTAAAGTTCAGTAGAATCTTCTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG  
 AACCACTTACTAACCAATTCACCCCCCAACCCCTTCTACTGCTACTTTAAAAAATTAATAGTTT  
 CTATGGACTGATCTAAGATTGAAAAATTAATTTCTTAATTTCAATTGAGACTTTTATTTACATGACTCTA  
 AGACTATAAGAAAAATCTAGGCAAGTGACAAAGTGTAGCATTATTGTTATTAATAAGCACTTTGGAGTATG  
 TGTGCACTTATAGTGTATCAGTTCTTGCAATGTATTTTGCCTTTGTTTAAAGCCTGGAACCTTTGAAGAAAT  
 GAAAAATTAATTTTCTTAGGACGAGCTATAGAAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT  
 TGGAAACCTTGCTGGTGTATGTATGTGCTCTCTGCTTTTGAATGACTTTATCATCTAGTCITTTGTCTATTTT  
 TCCCTTGTATGTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAATAAATGAT  
 TAAATATGTCTTTGAAAAAATAAAAAAATAAAAAA

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**FIGURE 38**

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSRSGSSSSRSLGS  
GGSVSQLFSNFTGSVDDRGTCCQCSVSLPDTTFFPVDRLVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTFPVVHPPPTPGSCGH  
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGlyWVAPLNTDGRLLLEYRlyNTLD  
DLLLYINARELRITYGQSGTAVYNNNMVYNMYNTGNIARVNLTNTNTIAVTQTLpNAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTeASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF  
MVCGLYATRMTMNRTEEIfYYYDTNTGKEGKLdivMHKMQEKVQSINYNPFdQKLYVYNDG  
YLLNYDLSVLQKPQ

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GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACCCCTGTCGTCCAC  
CCTCTCCCACTCCAGGGAGTGTGGTTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTCTTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATGGNGGCCGCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT  
CGGGATCACCTATTGGCCAGGTAGTGGTACAGCAGTTTACAACAACATGTACGTCAACA  
TGTACAACACCGGNNATATGCCAGAGTTAACTGACC

**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTTGTGACGTTGTGGAGATGCGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT  
 GGATACCATGTTTGTGTGGAAGTGCCCGTGTTTGTCTATGCCGATGCTGTGCTGTGCTGGAAC  
 AACTCCACATGTAACTAGATTGATCTATGCACTTTTCTTGTCTGTTGGAGTATGTGTAGCTTG  
 GTAATGTTGTATACCGAGAAATGGAAGAACAACCTGAATAAGATTCTCGGATTTTGTGAGAATG  
 AGAAAGGTGTTTGTCCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GTTTTGGCTATGTTCTATCTTCTCTCTCTTTACTAATGATCAAAGTGAAGATGAGCAGTGGA  
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAAAATTA  
 TTATTGGGGCATTCTTCATCCAGAAGGAACTTTACAACGTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGCGCTTTTGTTCATCTCATACAACCTAGTCTTACTTATTGATTTTGACATTTCATG  
 GAATGAATCGTGGTGTGAAAAAATGGAAGAAGGGAACCTCGAGATGTGGTATGCAGCCTTGT  
 TATCAGCTACAGCTCTGAATTATCTGCTGCTTTAGTTGCTATCGTCCGTGTTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTTCAGAAAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTG  
 CGTTGGTGCTTCTGTAATGTCTATCTGCCAAAAATCCAAGAATCACACCAAGATCTGGTT  
 TGTTACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACCAAGAAACAAATTGCAACCCAAGTCTACTAAGCATAAATGGCTACAAATACAAACAAGCAC  
 TGTCCCAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATATAGGCAATTAATC  
 TCTTTTGTGTGTGTATTTTATTCAGCATCCGTACTTCAACAAATGTCAGGTTTAATAAA  
 CTGACTTGAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC  
 ACTGGAGGATGGGGACGATGTTCAACGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
 GTTATTCTCTTCTTCACTTCATGCTTTTCTGCTTCACTTTATATCATGATGACCTTACC  
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
 AATCTCTCCAGTTGGATTGGCATCGTGTCTGATGTTTGGACACTCGTGGCACCACTTGTTC  
 TTACAAATCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAGAGTCCCACTTTGATTATTGC  
 TTATTTGAAAGTGAATTTCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGCTAC  
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTGTTATTTTCTTACCAA  
 TGGCATTGATATGTGATGAGAATGAATTCAGAGGAAAGTTTTATGAATATGGTGATGAGT  
 TAGTAAAAGTGGCCATTATTTGGGCTTATTCTCTGCTCTATAGTTGTGAATGAAAGATAAAA  
 ACAAAATTTGTTTGTACTATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATAAAA  
 GCAAAATGTATGGCTGCCTTTTGAAATATTGTATGTGTGCTGGCAGGATAGTCAAGAAAC  
 ATGGTTTTATTTTAAAAATTTATAAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA  
 AGGTTTTACCTTGATACGGAATTTACACAGGTAGGGAGTGTGTAGTGGACAATAGTGTAGG  
 TTATGATGAGGTGTGCGTACTAAATGAATAACGAGTAAATAATCTTACTGGGTAGAGA  
 TGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAAACTCATGAAGTATGGGTTTCAGT  
 GGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAGGATAATCATGGTTAGA  
 AGGAAGTGTGTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCCAGCACCGTAGCTCACCCTT  
 GGTAAATCCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA  
 GCTTGGCAGATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCCCTGTGGTC  
 CAGCATGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTGTCAGTGAGCAAGTCA  
 CGTCACTGCATCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATGAAATCAAGG  
 AGGCAAAATTTTGACAGGGAAGGAAGTAACCTCAAAACCACCTAGGCTTTAGTAGGCTATT  
 ATAAATCTAGTCAGGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATTA  
 GTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATATAGCATTTCTCTGACATTTAA  
 AAATAATTTCTATTCAAATACATGATATTTGATTTACACCTCATCTGTGATTAATTAATGT  
 GATGTGGAATGCTGGTCCAGCATGACCATTAACAGGTCAGAAGATGATGGAATGTTTT  
 AGAATAAACCTCCTGCTTATAGTATACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT  
 TTACTGCCATGTGAATGAAATATATAGTATTGTAACTTTCAACCTGAAATCAAGCAGT  
 ATGAGAGTTTGTATTTGTATGTGTCATAGTGTCTAATGAAGCTTTTAAATCTACAAAT  
 TCTTCTTTAAAAATATTTTAAATGTGAATGGAATTAACAAATCAGCTTAATTTCCCAACC  
 TTATTCGTGTGTAGACATTTGATTTCCAAATTTGAAATGCTGTGTTTTACTCTAAATAA  
 ATGAATTCAGAGAAAAA

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**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNEVWEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMLEFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSWIGI  
VLYVWTLVAPLVLNDRFD

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**FIGURE 42**

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNACGTTGTGGAGAT  
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAGTAGATTGATCTA  
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCTTGTAACATT  
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT  
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCAATGGAT  
TTTGGTTCCTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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GTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTCCCCGTGTTTGNATGCCGATGCTGTCTAGTGGAAACAANTCC  
ACTGTAATTAGATTGATNTATGCACATTTTNTTGCCTGTGTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACCACTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGTGCAGTGCACAATGGATTTTGGTTTTTAAATTGTCTGCAGCAATTGCAATTATTATTG  
GGGC

AAGAAGCTGTCTCCACTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
 GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGAAGTGCCCCGTGTT  
 TGCTATGCCGATGCTGTCTAGTGGAAACAACTCCACTGAAC TAGATTGATCTATGCACCTT  
 TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACT  
 GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTGGTTG  
 GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCATGCTCTATCTTCTCTCTTTA  
 CTAATGATCAAACTGAAGAGTAGCAGTCTTAGACAGTGCAGTGCACAATGGATTTGGTT  
 CTTTAAATTTGCTGCAGCAATGCAATTATTATTTGGGGC

**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG

[illegible]

**FIGURE 47**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP  
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQVRKDLCQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY  
YGQGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ  
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRCLKHRGSSL  
HPFRKGLQEKKDKVWLLREQKRKKLRLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTYWCMRTINETHNLFCEEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

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AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCCTCTGGGGAGCACAGCCC  
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC  
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
 CCGAGTCCGCGGGGCCAGCCTTGCCCTTCCGGCGGGGGCCACCTGGGAATCTTTACAC  
 ATCACCGTCATCTGGCCAGGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
 CCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
 CGCTCGCTGAGGCTGCTGTGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG  
 TTCCACGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACAGG  
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC  
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
 GTGCTCTTTCCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG  
 ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
 ATCAGGCTGCTGCAGGCCTCTGCGGGCAGGGCAGCTGGGAGAGGCCTTGAGAATGTCCTTTT  
 GTTTTGGAGAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAGAAAT  
 AAAAAACCATAAGAAGCTTTAAAAA



**FIGURE 49**

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR  
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRRHPRHAR

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GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA  
CTACTGGGCTTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGC  
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCCTACACACCATCTGTGTCATCTGGCTGGCTACCCGCG  
TGTCCATCCTGCTCCTTGACACCTACATCAAGGACGGGAAGCTGTGTCCTATCCTCGGCTGG  
AGATCTACAGGAAGACAGATCCATTTCTATGTGCCCACTGGCACGCGAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCGACGCGAGCACAGCTACACGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTACGCGCTGGACCTGGGACTGAGC  
CCCTGGGGACTACCAAGTGGCTCTGGGAGGCCACTGCCCTGAGAAGGGCAAGGAGTAACCC  
ATGGCCTGCACCTCTCTGCAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCTTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA  
GGAGCTATTGTTCTGCACACGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC  
ACAGTGTAGGCTCCAGGACCCAGAATAAGGCCAATGATTACTTGTTTACCTGGAAAAAAA  
AAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATRVRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCP<sup>1</sup>LAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETS<sup>2</sup>AATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGE<sup>3</sup>GFLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

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**FIGURE 52**

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCAGTCAATGACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGTGCTTTTGGA  
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGCTGAGCAGA  
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTCTGCCTCTGGTAG  
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAATA  
ATAAATAATAAATTTAAAAAACTAAAAAAAAAAAAAAAAA

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**FIGURE 53**

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNKSKKK

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**FIGURE 54**

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCAGTCATGACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGCTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTAAAAAAGCTTA

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGAAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAATAATAAATTTTAAAAAACTTAAAA

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**FIGURE 56**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTGTGTTTCTTGGCTAAAATCGGGGAG  
 TGAGGCGGGCGCGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
 ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT  
 TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTCAACCACTCATACCATGCCT  
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG  
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG  
 CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT  
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT  
 TTCCACAGCACAAACAGCCCTGCATGGGTTGTTTGTGTTTTTACTGCTCACTCCCAACCTT  
 TTGTAATGCCATTTTCTAAACTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
 AAAATCACGAGAACCTTAAACAACAACCAAAAAATCTATTGTGGTATGCACCTTGATTAACCT  
 ATAAAAATGTTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT  
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTGCATA  
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTAAATGTGTTATTCAAATGTGGT  
 CTCTTCTGTGTCAAATGTTAAATGAAATATAACATTTTTTAGTTTTTAAATATTCCGTGG  
 TCAAAATCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT  
 GTAACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTGGAAGAGAGAAGCACCAT  
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT  
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
 CACATCCACCACTG

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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFGTGWIIIDAAVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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TTCTTTGGCTAAAAATCGGGGAGTGAGGCGGGCGCGCGCGACACGGGGCTCCGGAAC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATC  
CTCAGAATGCATTGACTGGGGGGAAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCCTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAAACGGTG  
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATT  
TTCCAGAATGCCTTCATCTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATAACC  
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT  
ATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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**FIGURE 60**

GGACACCGGGTTCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTNNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAAAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTGGATTT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

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**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAATCGGGGGAGTGAGGCGGCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGA CTGACCTGAAAAAATGTTTG  
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

CGGCGTAAATCGGGGGAGTGAGGCGGCCCGGCGCGG

**FIGURE 63**

CGACGCCGGCGTG**ATG**TGGCTTCCGCTGGTGCTGCTCTGGCTGTGCTGTGCTGGCCGCTCC  
TCTGCAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCTTTCTCCGAAGATGTC  
AAACGCCGCCCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTCTCTCAAAACAGC  
TTTTTTCAGCCAAACCAAGTGCCCGGAGAACTGGATGTGGTGGTAAATTTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTCTGGAACAACAT  
ACCAAGGCGAGGGGGTGTGTCTATACCTTTGGAAAGAAATGGGCTTGAATTTGACACAGGAAT  
CCATTACATTGTGGGCTGTGGAAGAGGCGAGCAATTTGGCGGTTTTATCTTGACACAGATCACTG  
AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAGAGTACCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGGCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCCGTGGTTCAGCTCCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCCTTCAAGCATCCACCCAGAGCTGGCTGA  
GGTCTGCGAGCAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGTGTCAACCCCAACCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC  
ATGAAAGGAGGCTTTTATCCCCGAGGGGGTCCAGTGAATTTGCCTTCCACACCATCCCTGT  
GATTCAGCGGGCTGGGGGCGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTGTGCTGGACT  
CAGCTGGGAAGCCTGTGGTGTCAAGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCGTGGTCTCAACACAGGACTGTTCACACCTATGAACACCTACTGCCGGGGAAACGC  
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCGGCTAGGCATGACCT  
CTGTTTTCATCTGCCTGCGAGGCCAACGAAGAACCTGCATCTGCCGTCCACCACTACTAT  
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGTCACTGCTCCATGCCACGGAAGTA  
GGGTGCGGAACACATCCCTCTTCTCTTCTTCTCGCTTTCCCATCAGCCAAAGATCCGAGCTGGG  
AGGACCGATTCCCAAGCGGTCCACCATGATCATGCTCATACCCACTCCGTACAGTGGTTTT  
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGCAGTGACTATGAGACCTTTCAAAAACCT  
CTTTGTGGAAGCCTATGTCTAGTGGTGTCTGAACTGTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGACTGCAGGATCCCCACTACCAACCAAGTCTTATCTGGCTGCTCCCGAGGTGCC  
TGCTACGGGGCTGACCATGACCTGGGCGCGCTGCACCTTGTGTGATGGGCTCCTTGAAGGC  
CCAGAGCCCCATCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTCG  
GGGCGCTGCAAGGTGCCCTGCTGTGCGAGCAGCGCCATCTGGAAGCGGAACTTGTACTCAGAC  
CTTAAGAATCTTGATTTCTAGGATCCGGGCGACAGAAGAAAAAGAA**TAG**TTCCATCAGGGAGG  
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCTTGTGACGTATAAAGCACTCTAATTTGGTCTGATGCTGAAAGAGAGGCCCTAG  
TTTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG  
TCTCATGACAGCGGCGCTCTGCATCCCTACCCATGCCTCTCAATCAGTGATCAAGCGCA  
ATATTCCATCTGTGGATAGAACCCTTGGCAGTGTGTGTCAGCTCAACCTGGTGGGTTCAAGT  
TGTTCTGAGGCTCTGCTCTCATTTCACTTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG  
GAAAAGGGAGACTAATGAGGCTTAACTCAAAACCTGGGCGTGGTTTTGGTTGGCATTTCCATA  
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAAGTGGCTCTTCAAGGGGACAGGAAT  
GCCTGTGTCTTGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTGAGATGATCATATCCAATTCAATGGAAGTCCCGGCTCTGTCTTCTTATCA  
TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGGAAGTCACTGACTGAGCCTCAATCAAGC  
CTTATCCACCAATACACAGGGAAGGTGATGCAAGGGAAGGTGACATCAGGAGTCAGGGCA  
TGGACTGGTAAGATGAATCTTGTCTGGGCTGAAGCAGGCTCGAGGGCAATTCAGCCAAAGG  
CACAGCAGGGGACAGTGCAGGAGGAGGTGTGGGTAAGGGAGGGAAGTCAATCAGAAAGGGA  
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGAGTTAATAGCACATGTGAGGG  
TTAGACAGGTAGGTGAATCAAGCTCAAGGTTTGGAAAAATGACTTTTCAAGTTATGCTTTT  
GTATCAGACATACGAAGGTCTCTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG  
ATTCCATTGCTTTAAAAA

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**FIGURE 64**

MWLPLVLLLA VLLLA VLLCKVYLGLFSGSSPNPFSEDVKRPPAPLVT DKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGL EFD TGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLT KATVQSVLLDSAGKACGVSVKKGHEL VNIYCPIVVS NAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRG TKEDLHLPSTNYYVYD TDMDQAMERYVSMFREEAAEH  
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFE EWQAE LKGKRGSDYETFKNSFVEA  
SMSVVLKLF PQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNL YSDLKNLDSRIRAQKKKN

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**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
 GGGGTTGGCACCGGCCCCGAGAGGAG**GATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG  
 TGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT  
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGATCTGAATTAGAATCCTCTATTCAAGA  
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG  
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG  
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA  
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTCTACAACCT  
 ATGACTACAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGCTGCTAAGAGA  
 CGGCAGATGCAGGAAGCAGAAATGATGATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA  
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC  
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC  
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAGGCTCTTGTAT  
 ATTATACATTTGGAGCTCTTGGGGGCAATCTAATAGCCACATGGTTTGGTAAGTAGACTT  
**TAGT**GGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTT  
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAATATTCAGTTGAACCTCCTTCAA  
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA  
 ATTTTCTTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC  
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGCAGAATCATTTTTTACATTAGATTATCATAA  
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT  
 GAAATATTATACAATATTTTGAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT  
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC  
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC  
 CTATTTTGCTAATTTGTACTTTTCTTGTCTAATTTGGAAGATTAACTCATTTTTTAATAAA  
 ATTATGTCTAAGATTAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 66**

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD  
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQEAMM  
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK  
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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**FIGURE 67**

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT  
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCCAGGGGTGGGGTGTGAGATGGGTGCCCTCCCCTCTGCCTCCCATTTCT  
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVLAQLSCTLSPOHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPQPEDDADYYCSVGYGFSP

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**FIGURE 69**

GCGGCCCGCCCCGAGACCGGGGCCGGGGCGCGGGGCGGGGATGCGGGCCCGGGGGCGG  
 CGATGACCCGGGAGCGCAGCGCGGGGCCCGGCCCTGACCCCGCGCCCGCGCCGCTGAGCCCC  
 CCGCCCGAGGTCCCGGACAGGCCGAGATGACGCGCCGAGGCCCTGTTGTGCTGCTCGTGGCCGCG  
 CGCTGCTGCTGGGGGCCCTTCCACCGCGCGCGCGCGCCGAGGCGCCCCAAGATGGCGGAC  
 AAGGTGGTCCACCGCAGGTGGCCCGCTGGGCGCACTGTGCGGCTGCAGTGCCAGTGGATGGGA  
 GGGGAGCCCGCGCGCTGACCATGTGGACCAAGGATGGCCGACCATCCACAGCGGCTGGA  
 GCGCGTTCGCGCTGCTGCCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGCGC  
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGGACGCTGAGCGCTCAACTACACCTCGTCGT  
 GCTGGATGACATTAGCCCGAGGGAAGGAGAGCTGGGGCCGACAGCTCCTCTGGGGGTCAAG  
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTACACAGCCCTCCAAGATGAGGCGC  
 CGGGTGATCGCACGCGCCCTGGGTAGCTCCGTGCGGCTCAAGTGGCGGCGAGCGGGCACCC  
 TCGGCCCGACATCAGCTGGATGAAGGACGACCAGGCTTGACGCGCCAGAGGCCGCTGAGC  
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGGAGGACAGCGCAATAC  
 ACCTGCCGCGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAGGTGGATGTGATCCA  
 GCGGACCCGTTCCAAGCCGCTGCTCACAGGCACGACCCCGTGAACACGACGCTGGACTTCG  
 GGGGACCCACGCTCCTTCCAGTGAAGGTGCGCAGCGAGCTGAAGCCGGTGATCCAGTGGCTG  
 AAGCGCTGGAGTACGCGCGCGGAGGGCGCCCAACTCCACCATCGATGTGGGGCGCCAGAA  
 GTTTGTGGTGTGCCCCAGGGTGACGTGTGGTTCGCGGCCCGCAGCGGCTCCTACCTCAATAAGC  
 TGCTCATACCCGCTGCGCCGACAGGACGATGCGGGCACTGTACATCTGCTTGGCGCCACACCC  
 ATGGGCTACAGCTTCGCGAGCGCTTCTCTACCGTGTGCTGCCAGACCCAAATCCGCGGAGGCG  
 ACCTGTGGCTCCTCGCTTCGCGCACTAGCTTGCCTGGCCCGTGGTTCATCGCCGACCCAG  
 CCGCGCTCTCTTCTATCTTGGGCACTGCTGCTGTGGCTTTGCCAGGCCAGAGAAGCGC  
 TGCACTTCCGCGCTTCCCTCCTGCTGGCCAGCGCCCGCGGGAGCGCCGCGACCG  
 CAGCGGAGACAAGACCTTCCCTCGTTGGCCGCGCTCAGCGGTGGCCCTGGTGTGGGCTGT  
 GTGAGCATGATGGGTCTCGGCGAGCCCGCCAGCACTTACTGGCCCGAGGCCAGTGTGCTGGC  
 CCTAAGTTGTACCCAACTCTACACAGACATCCACACACACACACACACACACTCTCACAC  
 ACATCTACACGTGGAGGCAAGGTCCACACGACATCCACTATCAGTGGCAGCGGCCCGCT  
 ATCTGCACTGGGCACGGGGGGCGCGCCAGACAGGACGAGCTGGGAGGATGAGGAGCGAGCT  
 GCAGACGAAGGACGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGCACTGTGTGT  
 TGAGGCATAGCCCTTGACACACACACACAGACACACACACTACCTGGATGCATGTATGCAC  
 ACACATGCGCGCACAGCTGCTCCTGAAGGCACACGACACACCCATGCGCAGATGTGCTGCTGGACA  
 CACACACACACCGGATATGCTGTCTGGACGCACACACGTCAGATATGGTATCCGGACACA  
 CAGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCCCTGACACACACATGCACGG  
 ATATTGCTGGACACACACACACACACACGCGTGCACAGATATGCTGCTGGACACGCACT  
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACACGTCGACAGGCGAGATATGCT  
 GCCTGGACACACGAGATATGCTGTCTAGTCACACACACACGACAGATGCTGTCCGGACAC  
 ACACACGATGCACAGATATGCTGTCCGGACACACACACGACGACGACAGATATGCTGCTGGAC  
 ACACACACAGATATGCTGCTTCAACTCACACACGTCAGATATGCTGCTGGACACACACA  
 TGTGACAGATATGCTGTCTGGACATGCACACAGATATGCTGTCCGGATACACACG  
 CAGGCACACATGAGATATGCTGCTGGGCACACACTTCCGGACACACATGCACACACAGGT  
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCTTCAACTCACACACGTCAGATAT  
 TATTCCTGGACACACACATGTGACAGATATGCTGTCTGGACATGCACACACGTCAGATA  
 TGCTTCCGGATACACACGACGACACATGACAGATATGCTGCTGGGCACACACTTCCGGA  
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACACGAGCTGACGTGCTTTTGG  
 GAGGTGTGCGCTGCTGAGTACGTGTCGCTGAGGCTCATAGTGTGATGAGGACTTT  
 CCGCTGCTCCAGCTCACTCCCCAACTCTGCCCGCTCTGTCCCCGCTCAGTCCCCCGCC  
 CATCCCCCTCTGTGCTTGGCTTGGCGGCTATTTTGGCACTGCTTGGTGGTCCCGCAGG  
 AGTCCCCCTACTGCTGTGGGCTGGGGTGGGGGACAGCAGCCCAAGCCTGAGAGGCTGGAG  
 CCGATGGCTAGTGGCTATCCCCAGTGCAATTTCCCCCTCAGCAGAGAGAAGGGGCTTGGTA  
 TTTATATTTAAGAAATGAAGATAATATTAATATGATGGAAGGAAGACTGGGTTCGAGGAC  
 TGTGGTCTCTGTGGGCGCGGGACCCGCTGGTCTTTACGACATGCTGATGACCAACCC  
 GTCCAGGCCAGACACACCCCCACCCCACTGTCTGGTGGCCCCAGATCTCTGTAAATTTTA  
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAA

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MT P S P L L L L L L P L L L L G A F P A A A A R G P P K M A D K V V P R Q V A R L G R T V R L Q C P V E G D P P L T M  
W T K D G R T I H S G W S R F R V L P Q G L K V K Q V E R E D A G V Y V C K A T N G F G S L S V N Y T L V L V D D I S P G K  
E S L G P D S S S G Q E D P A S Q Q W A R P R F T Q P S K M R R R V I A R P V G S S V R L K C V A S G H P R P D I T W M K  
D D Q A L T R P E A A E P R K K K W T L S L K N L R P E D S G K Y T C R V S N R A G A I N A T Y K V D V I Q R T R S K P V L  
T G T H P V N T T V D F G G T T S F Q C K V R S D V K P V I Q W L K R V E Y G A E G R H N S T I D V G G Q K F V V L P T G D  
V W S R P D G S Y L N K L L I T R A R Q D D A G M Y I C L G A N T M G Y S F R S A F L T V L P D K P P G P P V A S S S A  
T S L P W P V V I G I P A G A V F I L G T L L L W L C Q A Q K K P C T P A P A P L P G H R P P G T A R D R S G D K D L P S  
L A A L S A G P G V G L C E E H G S P A A P Q H L L G P G P V A G P K L Y P K L Y T D I H T H T H S H T H S H V E G K V  
H O H I H Y O C

[illegible]

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI  
DYPGGKGDYERLDAIRFYYGDRVCARPLRLLEARTTDWTPAGSTGQVVHGSREGFWCLNREQ  
RPGQNCNNTYTVRFLCPPGSLRRDTERIWSWSPWSKCSAACQGTGVQTRTRICLAEMVSLCS  
EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK  
TPKLLTQTDSDGRFRIPGLCPDGKSIKTKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY  
MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG  
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPSYLIRLPHDCFQNNATNSFYDVGRCPV  
KTCAGQQDNGIRCRDAVQNCCKGSKTEEREIQCSGYTLPTKVAKECSCQRCCTETRSIVRGRV  
SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVL PFN  
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV  
KASVTFLDPRNISTATAAQTDLNFINDGDTFPLRTYGMFSVD FDEVTSEPLNAGKVKVHL  
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL  
DVPESRRRCFVKVRAYRSERFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA  
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHEDPR  
VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFN  
EDDPMSWTEDYLAWWPKPMFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS  
TRDRDQPNVSAACLEFKSGMLYDQDRVDRTLKVKIPQGSRRASVNPMLHEYLVNHLPLAV  
NNDTSEYTMPLAPLDPLGHNYGIYTVTDQDPTAKEIALGRCFDGTSDGSSRIMKSNVGVALT  
FNCVERQVGRQSAFYQLQSTPAQS PAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA  
QQPLIN

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**FIGURE 73**

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC  
 AATATCTTAACCTCTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCCTCTCATTTAAAAAAAATACAGAG  
 ACCCTACCTACCGGTACGCATACATACATATGTATATATATGTAAACTAGACAAGATCGCAGATCATAAAGC  
 AAGCTCTGCTTTAGTTTCCAAAGAGATTACAAAGAATTTAGAGATGATTATTGTCAAGATCCCTGTCGATTCA  
 CCCCTTTGGGTTACGGTGTCTCAGTGATGCGAGCCCTACCCCTTTGGTTTGGGGACATTATGATTGTGTAAGACT  
 CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCCTGCCACCGGAATCCACGGACATGACAAAAATA  
 TCTGAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTCGAGAGCTTCTGTGCCAATGGGCAATC  
 CCTACATGTGCATATAGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGGATTTT  
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTTGGAAGGATATAGTTATTACCTTTGAATCTGGCGCTCCAGACC  
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACAGACACATAGTTATTACCTTTGAATCTGGCGCTCCAGACC  
 AAATGATCTCGGAGAAGTCTCTCGATTATGGACGACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
 GATGCTTTTACATGGATCTAAATCCGTGAAGGATTTATCACGCATACGGTCTTAGAAATCATTTGCACAGA  
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGTTTCGCGCTTTTGG  
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT  
 ACAGTACAGACCTGAGGATAAGGCTTTAAGACCGAGCCGTTGGGGAATATTTGTAGATGAGCTACACTGGC  
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTTCCATGCCACTGTATGTC  
 TGTATGACAAACAGCAAAATGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG  
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCTATCTCCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC  
 CAGTATTTCCAGTATTTGTACGAATGTCTGCGACAACAGAGCTCTGCACTGCCAGAACGGAGGACGTGCCACA  
 ACAACGTGGCCTGCTGTGCCCCGGCGCATACACGGGCATCTCTGCGAGAAGCTGCGGTGCGAGAGGCTGGC  
 AGCTCGGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGGCACCCACGCGCTGCTGCTGCTGACCCGCTGCT  
 GGGAAACCGCCAGCCCCCTGGTGTGTTCTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCGGTGGGGAAGCA  
 GACACAACCCAAACATTTGCTACTAACTAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAA  
 CTAAGAAGGCTTAAGTGAACATAGCCATATTTATCACCCGTGGACAGCAGATCCGAGTCAAGACTGTAATTTTC  
 TGACTCCAGAGGAGTTGGCAGCTGTGTATATTACTGCAAAATCACATTTGCCAGCTGCAGAGCATATTGTGGA  
 TTGGAAGGCTGCGACAGCCCCCAAACAGGAAGACAAAACAAACAAATCAACCGACTAAAAACATTGGC  
 TACTCTAGCGTGGTGGCCCTAGTAGGACTCCGCCAGTGTGTGGACCAACCAATAGCATTTCTTGTGTGTCAG  
 GTGCATTGTGGGCAATAGGAATCTGTACAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
 CTGTGCTTTAGTGAACGTGCTCTGTAAACCTCGTTGGTTGAAGATTTCTTTGTCTGATGTTAGTGATGCACA  
 TGTGTAAACCCCCCTCTAAAAGCGCAAGCCAGTCTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA  
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTTGATTTCAAATGAAGTT  
 ATTTTTCTTGACTACTGTAATATGTAGATTTTTGTATTATTGCCAATTTGTGTTACACAGCAATCTGTTAAT  
 GTAICTATTTGCAATCAGCAAGAGCTGACATTTTATTTGTCTCTCTTCCTGTTCTGTTTTGTTTCACTGTGCGA  
 GATTTCTCTGTAAAGGCAACAGCTGCTGGCATCAAGAATATCAGTTTACATATATAACAAGTGTAAATGA  
 TTCCACCAAGAGGCTCTAAATGTTTTCTGTGTGCTTTAATCTGGAAGATTTAAAGAAATAAAACTCCCTGCA  
 TAAACGATTTCCAGGAATTTGTATTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAATTTCACTCACT  
 TTACTGATTTCTGTGGAGCTGAGTACATTCAGCTGACGAATTTAGTTCACAGAGATGAGTTGATGTTCACT  
 AGCTTGACACACTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACACGCAAAAAA  
 AAAAAA

**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVIDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCEEHNTTGPDCKGCKKNYQGRFWSPGSYLPKPGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF

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**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGTCCGCTAAGATTGCTGAGGAGGCGG  
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT  
 CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC  
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA  
 AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
 AGTATACATTTTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCTGTGGTGGGAATTCACAGCTTCCTATGACA  
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTGAG  
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAATAAAT  
 TCAGGAGGAGCTCAAGTTCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA  
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
 CATTTCGAGGAGTTACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
 TGGACCAAACTCG**TGA**GCCAGCCACCCCTGACCCAATGAGGAGAGCTCTGATTCCTCCAT  
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAATCTCATCAGCAGGGAGCCTGTGGA  
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGGGAAACATCTGCCCATGTGTATTG  
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATTCTAT  
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT  
 GCTTCAGAAGTGTTATTTTCAATGATCATTATATGATTTGATCCCCAGGATTCTATTTTGT  
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT  
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT  
 TTGTAACAATAAATATTTTGGAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC  
 TAAACTTGTATAAAAGTGTTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAATG  
 AAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTATTAATAAAAAAAAAAAAAAAAAA  
 AAAAG

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**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSF GDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLIILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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10011 10011

**FIGURE 77**

TGCTTCCTGGAGACCCGTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAATAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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CTCAGCGCGCCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAACCGTAGCGCGCA  
CCCCGACCTTAAAGAGCTGGGGAGCAAGAGGAGGACAGAGCCCTTTAAACACGAGCGGGGTGGTG  
CTGCTCCCTTTTAAAGCGGGGGCTCCGGACAGCTGTAFTCTGAGCCCCAGACTGCCCCAGTT  
TCTGTGCGAGGCTGCGAGGAAAGGCCCTTAGGCTGGGTCTGGGTGCTTGGCGCGCGCGGCTT  
CCTCCCGGCTGCTCTCTCCCGGGCCAGGACCTCGGCTTCAGTCATGCTGAGCAGATA  
TGGAAGCACTGACTACGAAGTGCATTCGCTGCGAGAAGCACTATTCCAGAGAGGACTCCG  
GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCTCTGCCACATCTTCTCTGAC  
CCGCTTCAAGAAGCGCTGCTGAGTTTACCACAGCTGGATGATGAAGATGCCACCTCAACAAGA  
TTGCGCTCGAGCTGTGACCTTTACCTTGCAATTGCGCTGGGTGCTGTCTGCTCTCTGCGC  
TTCTCCATCATCAGCAATGAGTGTCTGCTTCCCTCTCCCTCGGAACACTACATCATGCTGCA  
CAACGGCTCCCTCATCCATGCGCTCTGGAACCTTGTTTTCCTCTCTCCCAACCTGTCCCTCA  
TCTTCTCATGCTCCCTTGCATATTTCTTCTACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG  
GGTGTCTGGGCGGGGTCTATGAGACAGTGGTGATGTGTGATGCTCTCTCACTCTGCTGGTGTCT  
AGGATGGTGTGGGTGGCATCAGCCATGTGGACAAGAACAGGCCAACAGAGATGACTCT  
ATGACTTTTGGGAGTACTACTTCCCTACCTCTACTCATGCTATCTCTCTTCTGGGTGCTCTG  
CTGCTCTGGTGTGTACTACTCTGGTCTCGCGCCGATGTTCTCCGTACCTGGGAAGCTGCT  
AGTCAAGCCCGGCTGCTGGAAGACTGGAGGACAGCTGTACTGCTCAGCCTTTGAGGAGG  
CAGCCCTGACCCCGAGGATCTGTAATCTACTTCTCTGCTGGTGCCTTTAGACATGGAGCTG  
TTACACAGACAGGCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGGCGGCAAGGC  
TTCAGCCTTGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTTGCTGGTGTGCTGACGG  
GCCTGTCTGTGCTATTGTGGCCATCCACATCTCGTGAGGCTGTCTCATGATGAGGCTGCCAT  
CCCGAGGACTGCGAGGGTACTCTCTTAGGCCAGGTCTCTCTTCAAGCTGGGCTCTTTGG  
TGCCGTCTTTCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCTCAGTGTGGGCTCTTATA  
GCTCTCCACTCTTCCGAGAGCTGCGGCCCCAGATGGCACGACTGCCATGACGCAGATAATT  
GGGAACCTGTGCTGTCTCTGCTGCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGG  
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGAAGCTTCAACTGCTGGGCAATTTTCA  
TTGTGTTCTCTTCAACGACGCTTCTGAGCCTTCCACACACTGTGCTGTGTGGAAGCACTT  
ACTGCACTGTGCGGGCAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCGTGCCCTG  
CTCCGGTTTCCCCAGGCATCTAGGAAGACCAGACCAAGTGAAGCTCCAGCTGGGGGTGGGA  
AGGAAAAAATCGACACTGTCATCTGCTGCTTACGCTGAGGGAAGCCCAAGGCTACTTTGG  
ACCTCAGGACCTGGAATCTGAGAGGTTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATATT  
GCATAATCTGAGCCAGAGTTTGGGACAGGACCTCTGCTTTTCCATACTTTAACTGTGGCT  
CAGCATGGGTGAGGCTGGGTGACTGGGCTAGGCCCTGATCCCAATCTGTTTACACATCA  
ATCTGCTCTACTGCTGTTTCTGGGCCATPCCCATAGCCATGTTTATCATGATTTGATGTCGAAT  
AGGGTGGGTAGGGCAGGAAAGACTGTGCCAGGGAGGCTGCGGAGATAGATTGTCTTCC  
CTTGCTCTGGCCAGCAGAGGCTAAGCACTGTGCTATCTTGAGGGGCTTTGGACCACCTG  
AAAAACAAGGGGATAGGAGGAGGAGGCTTACGCCATCAGCAATAAAGTTGATCCAGGGA  
AAAAA

**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDATVVK  
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMSVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPDLMELLHRQVLALQTVLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLI FYLMVSSVVGFY  
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY  
IVFLYNAAFAGLTTCLVKTFATAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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GGCTGCCGAGGGAAGGCCCTTGGTGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC  
GCTCGTCTCTCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACAGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTGTGTTTGCAACTGTACATCTCTCGCAGACTTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTACACACAGTGGAATGATGAAGATGCCACCG



**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCCGAGGAAAGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

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**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCCATGCTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCATT  
ATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA  
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTGAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTTCAGAGATGGGATTTCC  
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTTGT  
 GAGGCGGCCCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGGGCGGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT  
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
 GGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA  
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCCTTGGGGATTT  
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA  
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTGTGCGCAAGAGAT  
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTACGGTTCGGAATCAAAGTTGTCAAGCACCCAAATATTTGAAGGAGAGGAGATGATT  
 GTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTCAGAGTG  
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTTGTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGCAATTCGGAAGAAGATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCCCTGAGT  
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAACACAATATAGAGGGTTGGA  
 GTTGTGTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGT  
 TTATTTTTTA

**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ  
AQEKFDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ  
DRNI PRGSDI IVDLEVTLEEYVAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
MTQEVVCEDECPNVKLVNEERTLEVEIEPGVRDGM EYPFIGEGEPHVDGEPGDLRFRIKVVKH  
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHK VHSRDKITRPGAKLWKKGEGLPNFD  
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTGGAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG  
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG  
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTNTGTGAGATAGTGAGAAACGGAACA  
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

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**FIGURE 87**

GGCACGAGGCGGGCGGGCAGTCGCGGGATGCGCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
 CTCTGCAGGTGTCTGTGGAGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA  
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATTCTTTGCGTTCGTTTGAGCC  
 TTGGTGTGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
 TAAGCCCATTTGTGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
 TGGACGATGTCTGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC  
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
 GCGACATCATTTGTGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
 TACCCTCCGTGGACCCAACTCCTGGACGCACGGACGACTGCCTGTCTCTGTCTGTGACG  
 TCACCTGGTGTGTTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC  
 AGTCTCTGTGGGTGCTGAGGAGCATTGGAAAGTCCCTCGAGAAGCAGCCCTAGCTTCTGAG  
 CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATT**TAGT**GCCT  
 ACAGGCCAGCAGCTAGCCATGAAGGCCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT  
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG  
 TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTGTCAGTTGCAAACTGTGGCTGGTGAGT  
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTGCAAGAGGAGTATTGAAAA  
 CTGGTGGACTGTGAGCTTTATTTAGCTCACCTAGTGTTTTCAGAAAATTGAGCCACCGTCT  
 AAGAAATCAAGAGGTTTACATTAAATAGAAATTTCTGGCCTCTCTCGATCGGTGAGAATG  
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC  
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTGTTATTATCTGCCT  
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAT  
 ACAAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
 GATAGTAAATTTATACTTATGTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC  
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA  
 TTTGGAGTGTTTTTCTGTCTTTGGAATGATTCCTTTTTTACAAAGCACTACTGGCTAT  
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTCAGAT  
 TCTTCTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTGTAGTC  
 CTTATTGGTTGGCCTTGTATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTGTTCAG  
 GGGCTTCTTCCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA  
 AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG  
 CCTACAAAGTACCAGCAGCAAAATAGCAAAGAAGCAGTAAAACAGGCTTCTACTCAAGTGA  
 ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
 ACTCTTGAAGCTATTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
 CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
 TTTTAGAAGTGCCACTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA  
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG  
 ATGTATGGATTACTTTTTTTGNGCNCAGGGCC

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 10611 12660

**FIGURE 90**

MISLTDTQKIGMGLTGFGVFLEFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLP  
RSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

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**FIGURE 91**

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTCTGTTCTTTGGA  
ATGATTCTCTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT  
GGCTTTTGTAATTGTTTTAGAAAGAACATTAGATTCTTCTTCCAAAACATAAAATGAAAG  
CTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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GGCACGAGGCTGAACCCAGCGGGCTCCATCTAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG  
GGCTGCCAGGAAGGAGACGCCTTCTGAGTCTGGATCTTTCTTCTCTGGAATCTTTGA  
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC  
TGAAGTCTCAGTTCTCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC  
ATCAACACCATTACGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGTCTGTGGAGTGGTGGT  
GGGGCACGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT  
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCGGGAGTACCCCGAGAAGTATTTTTCTT  
GATTCACTGTGAGGCGACACGGTTTACCGGAGAAGAGACTAGATCAGCATGCAGTGGCCG  
GGCCAGTGGGCTGCCTCGCTCAAGCATCAGCTTCTTGGCAGAACCAAGGGCTTGCGCATC  
ACCGTGAGAGAGCTTGAGAAATGTAGTTTCAAGCTGTATATGACTGTACACTCAATTTAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTGTATG  
TTAGGAGGATCCCCTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCCTGGCTGCAC  
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA  
GACGCCCATGGTGCCCCCGCGCGCCCTGGACCTCTGTGAAGTGGCTGTTTGGGCCTCGC  
TGGTGCTCTACCTTTTCTCCAGTTCTGGTTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACT  
**GA**CTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTACGA  
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAAATCTTT  
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGATATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGACCGAAGGGGACAAGTTCCCTTTTATCCTTTTGGTGTGAGTTTTCTGT  
AACCCTTGTTTCCGAGAGATAAAGTGAAGAAAGTCTTTTAGGTGAGATGACTAAATTATGCCCTC  
CAAGAAAAAATAATTAAGTGTCTTTTCTGGGTCAAAAAAATAA

**FIGURE 93**

MDLAGLLKSQFLCHLVFCYVFIAAGLIINTIQFLTLLWPINKQLFRKINCRLSYCISSQLV  
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK  
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRIPILEDIPEDDDECSAWLHKLYQEKAQEEYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWRMIGVTEIDKGSAYGNSDS  
KQKLND

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**FIGURE 94**

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTGGGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA  
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATTCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAACCTTGCAAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTCTGAACACTGGGTTATAAAAC  
 TGTATCAGGTTCCGTATGTCCACTGGTTTTAGCCGAGCAGTACAACACACAGCTCTAAAT  
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGATGCTTCATTA  
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT  
 AGTAAAGGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG  
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTCAGGCATTA  
 CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTCATGTGTTATGCTTTAAAAATAGACA  
 TGTTTCTAAAAGTAGCTGTAACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTACAA  
 TTT**TGA**TCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTAAGTTCAATTTGTTTTTACTATGTTAC  
 CTGTTTGCAAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
 ATCAGATGCTTTTTATTTCCAACCTTTTTTTTACCTTTTCACTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTTCTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT  
 TTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG  
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLLEVKGEAKNSITDSQMDDVEVVYTIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRQWFKRSRLDQTQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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**FIGURE 96**

GGCACAGCCGCGCGCGGAGGCGAGAGT CAGCCGAGCCGAGTCCAGCCGAGCAGCGGACCAGCGCAGGGCAGC  
 CCAAGCAGCGCGCAGCGAACGCCGCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTCCCT  
 CCTTCCCCCGGTCCCCGCTCGCCGCGCCAGTCAGCTTGCCTGGGTTCCGTGCCCGCGAAACCCCGAGGTCAACA  
 CGCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCGCTCCACGCCCTCCCTTCCCTTGGCCGCGGCGCTGGCACC  
 GGGAGCGCTTGCTGACGCGAGGCCAGCTCTACTTTGGCCCCGCTCTCTCCGCGCTGCTCGCCTCTTCCAC  
 CAACTCCAACCTCTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGGCGCGCTCGCGTAG  
 CGCCGCTTCCGCTCGGTCGCTCAAAGTGGAAAGCGCTCCGCCCGCGCCGACCATGGCAGCGTTGGCTTGGC  
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGCTGCCAGCTCAAGTGCAAAAGTTGCTCGG  
 AAGTGGCAGCTCTTTACGTGTCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
 TTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCTGCCAAGTAAAGA  
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTG  
 ATGAATCTTCAAAGAAGTACTTGAAGATGAGAGAATCCCTGAATGATATGTTGTGAAGACATATGCCCAT  
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT  
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGTCGCTCCTGGAGCGGATGTTCCGCTGGTGAATCCCACT  
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT  
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG  
 AGATCTGCTGAGCAAGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
 GCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAAACATCATGAGAGGCTGTTTG  
 GCCAACCAAGGGGATCGATTTTGAATGGAACAAATTTACATAGATGCTATGCTGATGGTGGCAGAGGCTAGA  
 GGGTCTTTCAACATTTGAATCGGT CATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG  
 ATAATAGTGTTCAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT  
 TCTCGTTCATCTCTGAAAGTGCTTCAGTGCTCGCTT CAGACCAATCACCCCGAGGAACGCCAACCCACAGC  
 AGCTGGCACTAGTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCT  
 CCTTCCGAGCAACGTTTGCAACGATGAGAGGATGGCTCGAGGAAACGGCAATGAGGATGACTTTGGAATGGG  
 AAGGCAAAAGCAGGTACTCTTTGTCAGTGACAGGAAATGGAATAGCCAACCGAGGCAACACCCAGAGGTCCA  
 GGTTGACACCAAGAACAGACATACTGATCTTTCGTCAAATCATGGCTCTTTCAGTGATGACCCAGCAAGATGA  
 AGAATGCATACAAATGGGAACGACGTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAAGGAAGTGGAAATGA  
 GGCTGTGAGTATCAGCAGTGCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGGCAATGA  
 GAAAGCCGACAGTGTGGTGTCCCTCTGGGACACAGGCTACCTCCTCAGTCTGCTCTGATCTTGTTCCTGG  
 TTATGCAAGAGAGTGGAGATAAATCTCAAACCTCGAGAAAGTGTTCATCAAAAAGTTAAAGGCCACCAAGTT  
 ATCAGTTTCTACCTCCTAGTGACTTTGCTTTTAAATGAATGGCAACAAATGTACAGTTTCTACTATGTGGC  
 CACTGGTTTAAAGAGCTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAGGGACTGTGCATTGAGTTGGT  
 TCTTCTCTCCCCAAACATGTTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTGTGTA  
 TTTTCTACTCTTATTATGTTTGTATGTTTCTCATTTGTTTGTGGGTTTCTTTTCAACTGTGATCT  
 CGCCTTGTCTTCTAACAGCAACAGGCTCCTCTCTGGCAGTGAATGTACGTATTTCTGAAATATTAAATA  
 GCTGTACAGAGCAGGTTTTATTATCATGTATCTTATTAAAGAAAAGGCCAAAAGC

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**FIGURE 97**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFKELLENAEKSLNDMF  
VKTYGHLQMNSSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLKLVTRAFAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSAFRPHHPPEE  
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKKSRYLF  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE  
GSGSGCEYQQCFSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC  
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCTAGCTAGTGTATTAAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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**FIGURE 99**

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

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**AATG**GCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATCTGACCT  
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCC  
 AAGCCAGACTTCCCCAAATTCTAAGCCTCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
 GTTCATCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
 AACATTATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
 GCCAAATCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
 TCCC AACGAGTTCTCAGGATT CAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC  
 CTGACTGCATTTTGTCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG  
 ATGGAGAGGAAAAA

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**FIGURE 101**

MAVLVLRRLTVVLGLLVLF LTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIENAVE  
FILRSMSRSTGFMFDDNEGKHSSK

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**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGTCTTCTTAC  
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC  
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
 CTCTTCAGCCAGATAAAAGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG  
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCC  
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG  
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAATG  
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
 AGCCACCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT  
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTTGCCAGGGCAATCTCTAATTCAATC  
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC  
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATCGCT  
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT  
 CTCCCCACTACCACTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAATATTTTTTAATAAATAGACGA  
 AACCACG



GTGGGATTATTATTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAG  
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG  
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
TTAAGGAATGAGGTTACAGATTACAGGAATGTAGGGCCTCAACCTATAGACTTTGTCCCAA  
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGGTCATCGCTGCATCTG  
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACAGCACAACACTCGCTCCAAT  
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG  
TGATTCCTCGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAA  
AAGTAAAGGAGGATCTTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
TTGCCAATTCTGGTTCCCGAGCGCAAGAAGGCCATATACATGGATGATGATGATAATTGTGCA  
AGGTGATATCTTGCCTTTTACAATACAGACATGAGCCAGGACATGCAGCTGCATTTTCAG  
AAGATTGTGATTACGCCTCTACTAAAGTTGTCACTCCGTGGAGCAGGAAACAGTACAATTAC  
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCTGAAGCTTTCCATGAAAGCCAGCACTTG  
CTCATTTAATCCTGGAGTTTTTGTGTGCAAACCTGACGGAATGGAACGACAGAATATAACTA  
ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT  
GGTAGCATCACACACCTCCTCTGCTTATCGATTTTTATCAACAGCACTCTACCATCGATCC  
TATGTGAATGTCCGCCACCTTGGTTCAGTGCTGGA AACGATATTCACCTCAGTTGTAA  
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCATGGGGAAGGACTGCTTCATAT  
ACTGATGTTTGGGAAAATGGTATATCCAGACCCAACAGGCAAAATCAACCTAATCCGAAG  
ATATACCGAGATCTAAACATAAACTGAAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG  
GAAGTCTTGGAAGATAGCATGCGTAGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAGATGACAAACTGCCCTGTCTGGCAGTC  
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT  
ACTACAATCTGTAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA  
TAATTTCAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAATAAAACTT  
ACATTTTTC



**FIGURE 105**

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR  
QEEIPVVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK  
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDI LALYNT  
ALKPGHAAAFSEDCDSASTKV VIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA  
NLTEWKRQ NITNQLEKWMKLNVEEGLYSRTL AGSITTPLLIVFYQQHSTIDPMWNVRLGS  
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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**FIGURE 106**

TGTTTTTGGCCCATAAATCCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCACGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

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**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGCGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT  
TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCGGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTGGTCTCGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGCTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
ATGAAACCTTTAACTTTTGAAGGTTCTACTTGCCAAATCTGGGTTCCAGCGCAAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCACTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
TTCGTAAGCTTTCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC  
CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCGCCACCTTGGTTCAGT  
GCTGGAAAAAGCATATTCACTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA  
GACCAACAGGCAAAATTCAACCTAATCCGAAGATATACCGAGATCTCAACACATAAAGTGAAA  
CAGAATTTGAAGTGAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG  
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT  
ATGCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA  
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTGGTTTTTAATTTT  
GTAACCTGTGGCCTGATCTGTAATAAAAAGTTACATTTTTCATAGGTAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGACAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGAGCCATCTCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCACTCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCTGTCTGAGAAGGGCCCCACCACCCAGAGCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAAGTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
GCTGGGCCCTCCCCTGGTCTCCAGTGTGCTGGATAATAAATGGAACATATGGCTCTAA  
AAAAAAAAAAAAAAAA

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**FIGURE 109**

MGA AISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGFWPSLEPRT

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**FIGURE 110**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
 GTTCTCCAAAGCAAGTCATTTCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCAGTGGAA  
 TCATGTTCGGGAAGAGATACAATCCTTGCCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
 ATGATGTTTACCTTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTTCATTGGTTAT  
 TTTGGGATGTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
 TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGCATCGTA  
 TCCACAGGCATCAGCGCAGTGTCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
 GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCC  
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCGGGTCTCTGGGTGGCTGTGCTGCTG  
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCCCT  
 TTCGGGCATTCGGTACATGTGGTCGTACCATTAAATTGGCCTCATCTGGACTAGTGAATTCA  
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCACAGAAGT  
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA  
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA  
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
 TACTACAACCTGCTATTAATGGGACAGATTTCGTGTACATCAGCAAAAGATGCATTCAAATCT  
 GTTCCAAGAAGTCAAGTCACCTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTTCTA  
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC  
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT  
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
 CGTAAAAGGAGCAACAAATTAACAATGCAAGGCACAGCAGGACAAGCACTCATTAAGGA  
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGATAGATATCCCATTTAGGTATCTGTACCT  
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTATCTTCTCTCAAAA

MSGRDITILGLCILALALS LAMMFTFRFITITLLVHIFISLVILGLLFCVGLWWLYDYDNTDL  
SIELDTERENMKCVLGF AIVSTGITAVLLVLIFVLRKRRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQOMTITAGAVVTCYFNRSKNDDPHPI LSSLSILFFYHQGTVVKGSFLISVVRIPIRIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFL GKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFAYLVAH  
SFLSVFETVLDAFLFCFAVDLETNDGSSSEKPYFMDQEFLSFVKRSKLNNAARAQQDKHSLRN  
EEGTLOAIVR

**FIGURE 112**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCCTT  
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAGCCTAAGGGAAAAAGAAATATTCATTTCTG  
 TGTGGTGAATAATTTGAAAAAAAATTTGCCCTTCTTCAAACAAGGGTGCATTCTGATATTT  
**TATG**AGGAGCTGTTGTTCTCAGTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTGTGCTGG  
 TGACTGGAGTACATTTCAAACAAGAAACCGCAAGAAGATTAAAAGGCCCAAGTCTCACTGTG  
 CCTCAGATCAACTGCGATGCTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATG  
 TCCAGCAGGATGCCAAGACCCCAAAATACCATGTTTATGGCACTGAGCTGTATGCATCCTACT  
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTGAGGAGGGAAAAATACTTT  
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGGTGCCAATCGTT  
 ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA  
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC  
 ACAAAGCCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA  
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCCTTCTG  
 CTGCTTCTACCAACAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT  
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA  
 AAGGCAAGATCCTCAGGAGCTGCCCTCCAGAAAACCTGTTGGAGCGGATGTCAGCCTGGGGAC  
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC  
 TGCAAAATTGACTTGTCTTTTTAATTGATGGGAGCACCAGCATTTGGCAACCGCGATCCG  
 AAFTCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGCTCCAC  
 TGATGGGTGTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACTTCAAGACACACAG  
 AATTCTCGAGATTTGAAGACGCCATAGAGAAAATTACTCAGAGAGGGAGGACTTTCTAATGT  
 AGGTCGGGCCATCTCCTTTGTGACCAAGAAGTCTTTTCCAAAGCCAATGGAAACAGAGAGCG  
 GGCTCCCAATGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAGTGGAGGAGGCT  
 TCAAGATTTGGGAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA  
 AATGAGAAGCAGTCTGTGGTGGAGCCCAACTTTGCAACAAGGCCGTGTGCAGAACCAACAG  
 GCTTCTACTCGCTCCAGCTGCAGAGCTGGTTTGGCCTCCACAAGACCTTGCAGGCTCTGGTG  
 AAGCGGCTCTGCGACATCACCGCTGGCTGCGAGCAAGACCTGTTGAACCTCGGCTGACAT  
 TGGCTTGTCTGACAGCGGTCCAGCAGTGTGGGAGCGGGCAACTTCCGCAACCTGCTCCAGT  
 TTGTGACCAACCTCCCAAAGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTG  
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTGCAAGTACAGCAGCAAGCCTGACAT  
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCA  
 ACTCTGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC  
 ATCACCAGCGGAGGTCCTACGACGAGCTCCGGAATCCAGCCATGGCTGCCATCTGAAGGG  
 AGTGAATCACTATGCGATAGGCGTTCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA  
 CTCACCCGCCAGAGACCCTCTCTTTTGGACGAGTTTGACAACCTCCATCAGTATGTC  
 CCCAGGATCACCAGAATCTTTGACAGAGTTCAACTCAGAGCTCGGAAGTGAATCAGAG  
 CAGGCAGCACCAGCAAGTGTCTGCTTTACTTAAGTGTGGACCAACCCACCGCTTAA  
 TGGGGCAGCAGCGTGCATCAAGTCTTGGGAGGGCATGGAGAAACAAATGTCTGTTATTA  
 TTTCTTGGCATCTCTTTTTCATATTCAAAACCTTGGAGTTACAAAGATGATACAAACGT  
 ATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAATT  
 GTTTTCAAAATTAATGTCGGAATACAGTGCAGCCCTACGACAGGCTTACGTAGAGCTTTT  
 GTGAGATTTTAAAGTTGTTATTTCTGATTTGAATCTGTAAACCTCAGCAAGTTTCAATTTT  
 GTCATGACAATTGAGGAATGTCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATTTT  
 AA  
 AA



**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC  
PAGCQDPKYHVGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQFVTLMO  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQ  
RQDPGSAAFQKPVGADVSLGLVPKEELSTQSLFVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHTNLKTHNSRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVVKRVCDDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDII  
LNAIKRVGYWSSGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

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**FIGURE 114**

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA  
TCCTTTCCGGCTGCTCATCCCCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT  
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCGCCCCACTACAGTTTTTCTCTGACTCTAAT  
 TGATGCAC TGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAGAGTGGTTGAAG  
 TGCTCCAGGACAGCTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT  
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTCC  
 TCCCAGCCTTT CAGACCCCCACTGGCATGCCATATGGAACAGTGAAC TACTTTCATGGCGTG  
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC  
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTTCGGCAACACATTGATGTGCTCACTGGC  
 AAGTGGTGGCCAGGACGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG  
 CCATCCGGAAC TACACCCGCTTCGATGACTGGTACCTGTGGGTT CAGATGTACAAGGGGACT  
 GTGTCCATGCCAGTCTTCAGTCCTTGGAGGCTACTGGCCTGGTCTTCAGAGCCTCATTGG  
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
 GGCTCCCGGAATTCACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCT  
 CTTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT  
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTCTG  
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAAACCACTTCATCCACAACAATGG  
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTAC A  
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTC TACTCTCTCAAACGGAGCAGGTC  
 GAAATTT CAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA  
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACTTCCAAGTTGGCATTACTGGGACAGGTTTTTCCT  
 AGACTCCTCA TAA CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA  
 AATTGCTTTTGGCTATCATAAAA

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAAPDAHYFSFLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKI  
LPAFQPTPTGMPYGTVNLHLGVNPGETPVTCTAGIGTFIVEFATLSSTLGDVPFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWAQDAGIGAVDSYFEYLKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQYMKGTVSMVPFQSL EAYWPGQLSIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNIQGYTVEKREGYPLRPELIESAMYLRATGDPITLLEGRDAVESIEKISKVECG  
FATIKDLDRHKLDRMESFFLAETVKYLYLLFDPTNFHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAAHLCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT  
LFSPENHDOARERKPAKOKVPLLSGPSOPFTSKIALLGQVFLDSS

AATGTTACATTTTCTCTGGAACCTCTCTAGGCACCTCCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTTGGGCCGGCTCTAGAACAA  
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATGC**CAGACTTTCACAATGGTTCTAGAAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTGATTCCATGTTTGCCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCACGTGATCGCGCTGGAGA  
 AACAGTGTACTATTCTGTCGAATACCAAGGGGGAGTACGAGAGCCTGTACACGAGGCCACATCT  
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
 GAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCTTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCGAGTTTGAGTTT  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
 GGGTATTCAGTGCACCTAGAAACATGGAGCCAGGGGCTGCATACCTGTGAAGGCCGACA  
 CATTGCGTAGAGCCATGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GAGGAGGCCATTCCTCTGGTATCTGGCCCTGTTTGCCCTTGTGGCTTCATGCTGATCCTGTG  
 GGTCTGCCACTGTTCTGCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
 TGGTCTCCAGACACCTTGAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT  
 CTCAT**TAG**GTTTGCGAAGGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC  
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGTGCCACTTGCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCTTCGGTCTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
 GGCTTGAGAGGCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
 TGTTGAGTTCACTTCAAGCCCATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGTCCAGCCACACTGAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTCT  
 TGTTGGTAAAGTACAGAATTACGCAATAAAAGGGCCACCCTGGCCAAAAGCGGTAATAAAA  
 AAAAAA

**FIGURE 117**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIA PGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLT EGPECDVTDDITATVPYNLVRATLGSQTS AW  
SILKHFPN RNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREP GAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQFTVK AIGRYSAFSQTECVEVQGEA IPLVLALFAFVGFM LILV  
VVPLFVWKMRLLQYSCCPVVLPD TLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-43 and 134-137

**Tissue factor proteins homology.**

amino acids 92-119

**Integrins alpha chain protein homology.**

amino acids 232-262

09060734.11901

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGTCAGGGCCACATGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCACGGTGGCAGCGCGCTG  
GCTGCTCCTGTGGGCTCGCGCTCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG  
AATGTGGCCAGCGAGTGGCGCTTCAAGACCCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCTGCAACCAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTCCCC  
ATGTTTAGCAAGATTGCAGTACCGGTACTGGTGCCCATCTGCCTTCAAGTACCTGGCCCA  
GACTTCTGGGAAGGAGCCCACTGGAACCTTGGGAAGTACCTAGTAGCCCCAGATGGAAAGG  
TGGTAGGGGCTTGGGACCCAACTGTGTCTAGTGGAGGAGGTGAGACCCAGATCAGACGGCTC  
GTGAGGAAGCTCATCTCTACTGAAGCGAGAAGACTTATAACCACCGCGCTCTCCTCTCCACCA  
CCTCATCCCGCCACCTGTGTGGGGTGACCAATGCAAACTCAAATGGTGTCTCAAAGGAG  
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGAA  
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAACAAAAATGTGTGCAA  
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAACCTGGGACCAATGATTAC  
CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCTTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAAACCAAAAAATAACTTGTATCAAT  
AAAAACTTGCAATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTATTCTCTCTGTATTATTTTCTTCATTACAAAGAAATGCAAGTTCATTTCTCAAAA  
AACAAATACCTCAGCATATAAAATAAAATGAAAGTATCTCTCTCAAAA

**FIGURE 120**

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLSEKRYGSVSLVNVASECGFTDQ  
HYRALQQLQRDLGPHHFNVLAFCPNQFGQQEPDSNKEIESFARTYSVSPFPMFSKIAVTGTG  
AHPAFKYLAQTSKGKEPTNFWKYLVPADGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL



CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAGCGAGGCC**ATGG**GCTGTCTACGTCCGGATGC  
TGGCCCTGGGGAGGCTGTGCGCCGGGAGTCCGGGGGTCTGGGGGCGCGGGCCCTCTCT  
CGGAGTTGCGAGGAAGCGAGGTGTCAGGGTGTCGCCTTCTCAGTTCAGGAGAGGTGGATCG  
CATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTACAGGGTGCACAAAAGCATCTTA  
ACAGCAAGACTGTGGGCGAGTGCCCTGGAGACACAGCAGAGGGTCCAGAAAGCAGAGGCTT  
TTGGTGCTCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGGAGTGGACAA  
AGCTGCTTTCTGGGCTCTGAGCATTTGGCTCTGCAAAGGTGACCGGCTGGGCATGTGGGAC  
TAACTCCTATGCATGGTGTCTCATGCAGTTGGCCACCGCCAGCGGGCATCAITCTTGGTG  
TCTGTGAACCCAGCCTACAGGCTATGAACTGGAGTATGTCTCAAGAAGTGGGCTGCAA  
GGCCCTTGTGTTCCCCAAGAGCATTAAGACCACCGCAACTACTACAACGTCCTGAAGCAGATCT  
GTCCAGAAGTGGGATGCAATGCCAGCAGGGGCTTGAAGATCAGAGCTCCGAGATCTGACC  
ACAGTCACTCGGTGGATGCCCTTTTGGCGGGGACCTTGCTCCTGGATGAAGTGGTGGCGGC  
TGGCAGCAGCAGCGCAGCATGTGGACAGCTCAATACACACAGCAGTTCTGTGCTGCCATG  
ACCCCTACAACATTCAGTTTCACTCGGGGACACAGGAGGCCCAAGGGGGCGACCCCTTCC  
CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC  
ACCGAGCAGTGTGGGATGATCTGCCCAACCCCTTGACCATTTGCCCTGGTTCGGTGGCGAG  
GCACATGATGTGTCTGATGTACGGTGCCACCTCATCCTGGCCTTCCCATCTTCAATGGC  
AAGAAGGCATCGAGGCCATCAGCAGAGAGAGAGGACGACCTTCTGTATGTTACCCCGAGAT  
GTTCTGGGACATCTGAAACAGGACGACTTTCAGGCTATGACATCTCGAAGTGTGTGGAG  
GTGTCAATTGCTGGTGCCCTGCACCTCGAGAGTTGATCCGAGGCATCATCAACAAGATAAAT  
ATGAAGGACCTGGTGGTTGCTTATGAAGACACAGAGAAGCAGTCCCGTGACATCTCGGCATCT  
CTCTGAGGACGTTGTGAGCAGTAGGACGAAGAGCGTGGCAGAAATTAATGCTCACCGGAGG  
CCCGGATCATGAACATGGAGGCAGGACGCTGGCAAAGCTGAACACGCCGGGGAGCTGTGTC  
ATCCGAGGCTACTGGCTCATGCTGGGCTATCGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
GGATCAGGACAGTGGTATTTGACAGGAGGATGTGCBCACAATAAGTAGCAGGGCTTCTGCA  
AGATCGTGGGCGCTCTAAGGATATGATGATCTCCGGGGTGGTGAGAACATCTAACCCCGAGG  
CTCGAGGACTTTTTCACACACACCGAAGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA  
CGATCGGATGGGGGAAGAGATTGTGCTGCATCTCGGCTGAAGGACGGGAGGAGACCCGG  
TGGAGGAGATAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCGGAAGTACATA  
GTGTTTGTCAACAACTACCCCTCACCTTTCAGAAAGATCAGAATTAACATCAAGTTCGAGA  
CGAGATGGAACGACATCTAAATCTCG**TGA**ATAAAGCAGGACCGCTGTCTTGCCGCTGAAGG  
GACTCTCTGCTGTCAGATGCAACCTGGCTTTTATGCACTAGATGTCCCCAGCAGCCAGTTT  
TGAGCCAGCCGATCAAAATGTCAAGGAATTGACATGAACGAACTAAGAGCTCTGGATGGGTG  
CGGGAACCTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTCCCAGGCCCTCCCTCTGT  
TCCATCCCCACATTTCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTCTTT  
GAAAAAATCAAAAAA

**FIGURE 122**

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ  
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVF PKQFKTQQY  
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDDEVVAAGSTRQHLDQLQYN  
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFlyGTPTMFVDILNQPDFSSY  
 DISTMCGGV IAGSPAPPELIRAIINKINMKDLVVAYGT TENS PVTFAHFPEDTVEQKAESVG  
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEFPQKTEEAVDQDKWYWTGDVAT  
 MNEQGFC KIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGVKDDRMGEEICACIRL  
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
 314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCAACCCCTGTACCATTCGCTGGGTTCGCTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

0000734.11904

GAGCAGGACGGAGGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC  
AGGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCGCGGGC  
GTGGACGCTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
AGTGC GGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTACGGG  
TTCTGGCGCTTCATCCAGCTGACGCAATGCGCTCAGGATTCGTGCAACGCCAAGCTCAACCTC  
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGCTGGAGTG  
CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGTTACATCGCCGCCGGTCTGTAGCT  
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA  
GCTAATGTGACTGTGTCTTTCCTTCGCGGGCTGTGTCCAGGATGAATCTCTGACTCGGGA  
TGGAGCTAACAGGCCCAAGGTTACGCTCAGTGGCTCTGTGTCCAGGTTCCGCTGCTACCTA  
CTGAGCTTCCGCAACACGAGCTTACTTCTCCCTCGAATCCACCCCTGTGTCGGGCTGCCCTT  
CCAGAGCCCACGACTGTGGCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG  
ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAAGCTCCGAGACAGGGAGTAG  
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGTC  
CGCAGCAATTAGGGCAGTATCTTGCAAAAGGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT**T**  
**GA**GCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
CATACTTCTCTGTTCCACCAGTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTTCC  
CAGTATCCCAGCTTCTGCTGCGCTGGTTTTCGGGCTTTGGGAAATAAAATACGTTGTATAT  
ATTCTGCCAGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
TCCGCTTGTCCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCAAGGGGAAGGTG  
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCCTCTAGCCAGCCCTGGACTTTGGAGCGTGG  
GGTGGGTGGGACAATGGCTCCCACCTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG  
GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC  
CCAATTTCGCCCTATAGTGAGTCGTA

MDPARKAGAQAAMIWTAGWLLLLLLRGGGAQALECYSCVQKADDDGCSPNKMKTVKCAPGV DVCT  
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQCCAQDRCAKLNLTSLAL  
DPAGNESAYFPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAAANVTV  
SLPVRGCVQDEFCTRDVGTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSTVTSTSAFVRCTSTTKMPAFTSQTFRQVGEHARSDEEPLRTGGAAGHQDRNSG  
QYPAKGGPOOPHNKGCVPATTAGLAALLTLTAAGVALL

[illegible]

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVEVQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 128**

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTACTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACCTCCAATAAAACATTTTCCATCCAAA

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**FIGURE 129**

MKIPVLPVAVLLSLVLVLSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAPKADE  
FLNWHALFESIKRKLPFLNWDAPFKLKGLRSATPDAQ

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**FIGURE 130**

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCATTGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTATTTTT  
AGGTTCAAGGTTCAATTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTC  
TTCACTATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPPTQETGPKAMGDLSCGFAGHS

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**FIGURE 132**

GGGGAATCTGCAGTAGGCTCTGCCGGCGCATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCGAGAAGGAGTCAGGTTCAAATGGA  
 AAGTATTTATTGACCAAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAAAC  
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
 GACTGTACCGGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAAATTTAT  
 CCTACAGGTCCTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG  
 GCCATGGAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
 ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCGAATACACCAAAAAC  
 CAGGCTCGAAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
 GGATCACTGCAAAATACAAGTATCTGTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
 AACACCTCTTCTGTGTGGCTCACTGTGTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC  
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA  
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGAGTCAAGAGATTGCTGAAAGGGGAA  
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
 TCCCAAAATGTTGAAAATGAACATAAGTAGTCATCATAGGACCATAGTCTCTTTGTGGCA  
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCAITTTCTTAAGACCAATC  
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAAATTCGTCAITTTGGAAGTAGTACAA  
 CTCAATTGCTGGAATTGTGAAATTATTCAAGCGTGATCTCTGTCACTTTATTTTAATGTAGG  
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCAATAAATCTGTGTACTCAG  
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAGCCAAA

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MEWWASSPLRLWLLFLFLPSAQGRQKESGSKWKVFDIQINRSLENYEFCSQNCSCYHGVI  
EDLTPFRGGISRKMAEVVRRLGLTHYQITKNRLYRENDCMFPSRCSGVEHFIFILEVIGRLPD  
MEMVINVRDYPQVPKWEPAIPVFSFSKTSYHDIIMYPAWTFWEGGPAVWPIPYPTGLGRWDL  
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT  
LGKPAAKDVHLVHCKKYKLFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY  
NVTNRKGYDQIIPKMLKTEL

CACCCCTCCATTCTCGCC**ATG**CGCCCTGCATGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC  
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG  
AGGTCACTGTATGTGGCTGCACTGCCCTGGCTTCGAGCTGGTGATGCGGTACTGGGAGCC  
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
GACTATGCTGAGTCTATGGGGCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCAGACC  
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
TGGAGCTGCTGACAGTCTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT  
TTCCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**  
**G**AGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAAC  
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT  
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATTCTGAGTTTCAGCCA  
CTGAACTCCAAGGTCCACTTCTACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
TTCAGTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
CTGACCACTCCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCTCTGTCAACCGT  
GGCTTCCACTCCAAGAAGGTGGACAGGGTCTGAAGTTCACCGGTCAATGCTGTCCCTCCA  
GGCCCCAACCTTGCTCTACCACTCCGGGCCCTAGCTTCTGCACCTCCTTAGGCCCTGCTCTCT  
GGGCTCAGAGCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTCTCAAAAAAA

MAPALLLI PAALASFILAFGTGVFVFRFTSLRPLLGIPESGGPDPARQGWLAALQDRSILAP  
LAWDLGLLLL FVQGHSLMAAERVKAWTSRYFGVLQRSYLVACTALALQLVMRYWEP I PKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGLKQVYYHVLGLGEPLALKSP  
RALRLFSLRHPVCVEILLTVLWVVP TLTDRLLLAFLLTLYLGLAHLGQDQLRYLRAQLQR  
KHLHLSRPQDGEAE

amino acids 1-13

amino acids 58-76, 99-113, 141-159, 203-222

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCAGCAGGAGATTGCTGCGCTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGCTCTTTTTTCTGTTTTTCAGAGTAGTTACACAACAGATCTGAGTGT  
 TTTAATTAAAGCATGGAATACAGAAAAACAACAAAAACTTAAGCTTTAATTTTCATCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGTCTCTCCGACTACTCACCCCGAGTGTAAAGAACCTTCGGCTCGCGTGTCTCTG  
 AGCTGCTGTG**ATG**CGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCAGTGAGATCC  
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTT  
 CTGGTCATTCTGGTGACCTCCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCCATTATGGC  
 ATTCAGTGGGTAAGTGAAGTTTGGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT  
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACGTCAGTGGGTTGGGTTATATAA  
 TGTCAGAGATTTGGTGCCAAAGGATCTATGAAATGATGGGTACAGTAAAAACCCATCAAGTTT  
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGAGTGAACATTTCATATTCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTGTCATGCTAAGGAACACC  
 ACATGCCATTAT**TAA**CTTCACATCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
 GTGTTAAATAAAGTAGGTACTGTGAAAATTTCATGGGAGGTGAGTGTGCTGGCTTCACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTTGTGATTTATTAGTC  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAA  
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG  
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTATTG  
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
 TGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACCTGAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGAGACTTTGTTAAAT  
 ATTTTACTGTGGTAAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAAA

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**FIGURE 137**

▲ 附錄二 國際標準化組織 ISO 9000 系列標準

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来源: 1. 国家图书馆馆藏; 2. 上海图书馆馆藏

**FIGURE 138**

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTTACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAAT  
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

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**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDNNDNNAGSGQQSVSVNNEHNVANVDNNDNNGWDSWNS  
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

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CAATTTCTGAAACTAACTCGTGTGCAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG  
CTCATATATAGGAAAATCGCATATGGTCTAGTATTAATTTCTTATTGCTTACTGATTTTTT  
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAGCTTCAGAGAAGCTGGTTTGTTTACATG  
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT  
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT  
CCAGGAAATCTGCATAGAAACACTTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
TGGAAAAAGAAGTAGAAAAAGAAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA  
TTGAATCCGGATGGAACCTCAGCCCTTTCAACCTCGGTTGGATTTTCTCCAGCTCAACAGCC  
ATCATCACAAGAGAGTAAGAACTGAGAGCAATCAACCAATCTCCATTAATGTGAAGACAG  
TCAAAAAGAGAACCTGAGATAGACACAGCGTTCCAAGGCCCTTACAATGGTGTAAAGAAA  
GACAGCAAGAGAAGTAGAATAAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGCATCAG  
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
GCTCGAGATCAAGAAGCAGGTCGCCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT  
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG  
TCATAAAAGGAAAAAATCTGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
GAGAGGTCCCATAAAAGCAAGACCATTGGTGGCAGTCGTCAGGACATGGCAGGCACAGGCG  
CTGAATTTCTCTTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT  
ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCCTCTA  
GGTCTCTAGAACACTGAGGACAGTTTCTTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT  
AAAATGCCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
TGTGTATTGTTTATTGCTATAAGAAGTGGAGCGTGAATCTCTGTA AAAATGTATCTTATTTT  
ATACAGATAAAATGCGACAGCTGTTCTATTTAAAGTGTTATTGTGTTAAATGATGGTGTAAT  
ACTTTCTTTAACTGGTTTGTCTGCATGTGTAAGATTTTTTACAAGGAAATTAATAACAAT  
CTTGTTTTTTCTAAAAA AAAAAAAAAAAGT

**FIGURE 141**

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRRKVALQEAQLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ  
SKSRDHSDAAKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNATTATCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAGGGCTTCGCT  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTNTTATTGCTTACTGATTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAAACATTAGGCTTTTATACAGAAAAAGCCAAATGATGAATTACTG  
GAAAAGAAGTAGAAAAAGAAAAGTAGCTTACACAGAAGCCNAATTAAGAGCAAGGGGATT  
GAAATCCGGATGGAATCTCAGGCCCTTCAACCCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGCACGAGGCCCTCGTGCCAAAGCTTGGCACGAGGGTGACCCGCGTTCTCGCACGCGCT**CAT**GGC  
 GGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG  
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
 GGCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG  
 AGACCTGCCCTCAGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG  
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCTACTACTACAT  
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTCACGGTGACCTTCT  
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC  
 TCTGTCTGCCCTCACCTTTGCCCTTCCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG  
 GGAGGAGACCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGCTTAGAGC  
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG  
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCTCACCTTCCAGGCCCTGCGGCTGGC  
 CCAGACCCACCGGAGCAGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC  
 ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC  
 TTCTTGACACAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA  
 CTCTGGGCGCCTCTGTTGTGCTGGTGGTGTGCTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC  
 ACCTGCAGGCCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
 GAGCTTGCGAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
 TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTACTATCCCCGACCCATCCTCAGCC  
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCGCG  
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT  
 GGACGGCTGCCTGCCAGCTGCTGCGCAGCCTTTTCGGCCTCTACTTCCACAGCACTTGGCA  
 GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA  
 CTAGCCTGCCCCCTCTGTTTGCGCCCGCTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
 GCGGTTCCCTTACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG  
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
 GATTTTTAA

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**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV  
VREETLELGLEPGLASMTQNL EPLLKKQGW DWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR  
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVVRVYCYVT  
VVS LQYLTP LIILTINCTLL LKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI  
AGALGGLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

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**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT  
TGTTCCGATACAAGCACCCGNTTGGAGGAGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC  
CATGCTGGTGCAAGCG

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**FIGURE 146**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATATCTTCTTACGGGGCCCGTGATTATTAACTGGCTT  
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGGCTTAAAGGAGC  
 TTGGCTGGTTTGGGCCCTTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGG  
 CGCTTCTGTGTGCTGCTTGCCTTGGCTCAGTCTGCTAATACATTGACAAATGTGGGCACCTGCACCTTCTGT  
 TATTTCAGAACTCTGTAAAGGTGCCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG  
 TCCAGACGGCTGTGCGAGCTTCACAGCCACGGCTCCCTCCCAGAGGTTTCTGCAAGTGGCCACCATCTCCTTTAA  
 TGACAGACGAGCCTGGCCTAGACAACCTTGCCTACGTGTCTCGGCAGAGGACGGGAGCCACCATCAGCCCA  
 GTGGACTCTGGCCGAGCAACCACTAGGCGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA  
 AAAATAAATCGAGCTTTGACTGTTCTTTCGAAGGACAAAGACGGGAGTGCAGTTGCCAACCATGCCGACCAGG  
 GCAGGGAAATTTCTGAAAACACCCTGCCCCCTGAAGTCTTTCCAAGGTTGTACCACTGATCCAGATGGTGAA  
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGCCTCTCTATTAGGCTGGTGGAGGTAGCGAAAC  
 CCCACTGGTCCATATCATTTATCCAACACATTTATCGTGTATGGGTTGATCGCCAGAGACGGCCGGCTACTGCCAG  
 GAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCTCTCCTGCGG  
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCCGCAGCAGGAACAATGGACAGGCCCC  
 GGATGCCATCAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCGCTTGGAA  
 TAAAACTGGTGCACAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCAGCCGCAAGAG  
 TGCGGCTCATCTGATTACGGCCAGTGAAGACGTGTTCACTCGTCTGTCGCCAGGTTTCGGCAGCGGAGCC  
 CTGACATCTTTAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT  
 CCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTTGAATCTCT  
 CGGCATGACCGTCCAGGGGGAGCATCATATAGAAATGGGATTTGCCATCTATGTGATCAGTGTGAGCCCG  
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGTGCATTTTGTGAATGGGATGGGTGCAACTGACA  
 GAGGTGAGCCGGAGTGAGGCAGTGGCATTTTGAAGAAGACATCATCTCGATAGTACTCAAAGCTTTGGAAGT  
 CAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGAATCCAACCAACATGGCCCCACCCA  
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACGGTGCTGTATAACTGTAAAGATATTGTATTA  
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTATGAAGAATACAATGGAACAAACCTTT  
 TTTCAATCAATCCATTGTTGAAGGAACACGAGCATACAATGATGGAAGAATAGATGTGGTGATATTCTTCTTG  
 CTGTCAATGGTGAAGTACATCAGGAATGATACATGCTTGTCTGGCAGACTGCTGAAAGAATTAAGGAAGA  
 ATTACTCTAATATTGTTTCTGGCCTGGCACTTTTTATAGAAATCAATGATGGTCAAGGAAAAACAGAAAAA  
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTATCTTGTGAGTTTTATATTAAAGAAAGATACATTGT  
 AAAATCTGACGAAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTTCAAATAAATTA  
 AACTACTAGTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACACATTTGTTATATTTTCTATTTCAAT  
 AAAAGAGCTTAAACAACTAAATGATTGATTGTATACCCCACTGAATTCAGCTGATTTAAATTTAAATTT  
 GGTATAGCTCAAGCTCCGAAGGTACATTTATGGCCATTTTAATTTTCAAGTAAATATTTTTTAAATGCA  
 TTGCTGAGAAACGTTGCTTTCATCAACAGAATAAATATTTTTTCAAGTATAA

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MKALLLVLPWLSPAYINDVGNLHFLYSELCKGASHYGLTKDRKRSQDGCPCDGCASLTAT  
 APSPEVSAATISLMTDEPLDNPAYVSSAEDGQPAISVDSGRSNRTRARFFERSTIRSRS  
 FKINRALSVLRRTKSGSAVANHADQGRESENTTAEVFPRLYHLIPDGEITSIKINRVDP  
 SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDIIKLVNGMDISNVPHNYAVRL  
 RQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDSSFHVILNKSSPEEQLGIKLVKRVDEPGV  
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHLIQASERRVHLVVSQRVQRS  
 PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE  
 WDLPIYVISVEPPGVISRDRIGTKDILLNVGVELTEVSRSEAVALLKRTSSSIVLKALEV  
 KEYEPQEDCSSPAALDSNHNMAPSDWSPSWMWLELPRCLYNCKDGMILRRNTAGSLGFCIV  
 GGYEYNGNKPFFIKSIVEGTPAYNDGIRIRCGDILLAVNGRSTSGVIHACLARLLKELKGR  
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CCAAAGTGATCATTGTAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCAGCACCTTCTCTCCAGGCA**AATG**GTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACATGGTGGC  
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTCTACCACAATTTTGACTATAAACATGGGTACATTGATCCAGGTGC  
TCTCCCGAAGAGCCTGCTTTATPCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATACACCTG  
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTAC  
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCCGTGCTGGAGGCTGTGCAAGGCTGGGCTCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTT**TAGG**ATGATTAAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAGTCAAAATTAATCTTTTCCCAATGCCCACTAATTTTGAGATTC  
AGTCAGAAAATAAAGTTGCTGTATTATA

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**FIGURE 149**

MKILVAFLLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST  
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE  
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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GGCACGAGCCAGGAACATAGGAGGTTCTACTGCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCAG  
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG  
 GCCGCTGGGTGCTCATAACTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC  
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCTCCTT  
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACTGCTCACCTACTTCTGCCGGGCGTCCCT  
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
 CCAGTGCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGGCAGGCCCCAGGGTGGA  
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
 GGCAGGTCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCTTCTCTGCCG  
 AGCCAGACATCGGACTGGTTCGGTGCCAGGCTGCAAAACAGCCAAATGTCCGAGCAGCGC  
 CCTCAGAGTGGTGCCCCAGGTGGTGACCAAGATGAGGAGTACTGGCAGGTCCCTCGGAGA  
 GCCCCATCTTGCCTTCCCGCTCTACAGAGCAGCCCGCGTCTAGTGGAAGAGGAGTTTGGG  
 GGGTTCAGGATAGGGAATGGGGAGGTTCAGAGGACGCAAGCAGCAGCCATG**TAGA**ATGAACC  
 GTCCAGAGAGCCAAGCAGCGGACAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTTGA  
 GTTATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

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**FIGURE 152**

GGTCCTTAATGGCGAGCAGCCGCCCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAAGAAA  
CTAAATGTCAACAAGCCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC  
AGGCAAGGATGCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGCGCATGTCTTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
CTGGAGCCAAGTGCAGGAGCACCACCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC  
AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA  
TCTGAGGAGAGTCCTTTAGAGTGACAGGTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG  
GTCTTGATCAAACCTGCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTCTT  
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTCTTGCAAATGATATT  
GTCAGTAAAATAATCAGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAG  
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCACAAAAA

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**FIGURE 153**

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRGPRWCAVQGOVDEKFTL  
HYDCGNKTVTPVSPLGKKLVNTTAWKAQNVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQSFDFGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFFHYS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

**FIGURE 154**

GGGAAAGCCATTTGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTG  
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAAATCATGAACCTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT  
CCTCTCTCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC  
TTAGATAGGCTTATCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

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10614 1400

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**FIGURE 155**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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**FIGURE 156**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTGGTCTTA  
 CCTACGGGCCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC  
 AGAACTGGCCCTCCGTTTGCTCGTGCACTAACCAAGTTTCAGCAAGGTGGTGTGCACGGCGCCGG  
 GGCCTCTCCGAGGTCCCCGAGGATATCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCACT  
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTTCGACAACCTGGCTGCAGTGCATCCCTAGCGGGGCCCTTTGAATACCTGTGC  
 CAAGCTGGCGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCCTTTACGCCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT  
 TCCCTGAGATCAGGCCTGGCTCCTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTGATG  
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC  
 CAACCTGGGCCACAATAACCTCTCTTTTGGCCCATGACCTTTTACCCCGCTGGAGTACC  
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATCTCTGGGTAGCC  
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTGATGCTCCCAT  
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGAGCGACCTCGAGACCTCAACATTTCTGAGGGTGGATGGCAGAAGCTTAAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGTCGCCAATGGGACAGTGCTCAGGCCACGC  
 CTCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC  
 TTTTCAGACACTGGGGTGATACATGCATGGTGACCAATGTTGAGGCAACTCCACCGCTCG  
 GCCTACCTCAATGTGAGCAGCGGTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT  
 AACAGTGGAGACACCGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCTA  
 CCACGTCCACTGGTTACCGAGCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGCACAAGATGCAGACCAAGCCT  
 GGATGAAGTGCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC  
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCCG  
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGCGAGTAGTGCTGCCACAATTC  
 ATGACCATATTAACATAACACCTCAAAACAGCACATGGGGGCCACTGGACAGAAAAACAGC  
 CTGGGGAACCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTGAGACCCA  
 TACCAAGGACAAGGTACAGGAACTCAAAT**TGACT**CCCCCTCCCCCAAAAACTTATAAAAT  
 GCAATAGAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTGA  
 TATGCTTATATATTAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAAGA  
 CAAAAAGTCAAAACA

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MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT  
 RRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
 LNTLELFDNWLTVPISGAFEYLSKRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
 ISĖGAFAFGLFNLYNLGMCNIKMPNLTPLVGLLEELEMSGNHFPETRPGFSFHGLSSLLKLW  
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCILW  
 LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
 KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGTLNFSHVLLSDTGVTYTCMVNTVAGNSN  
 ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTRKRYKPVPTTSTGYQPAYTTSTTVLIQ  
 TTRVPKQVAVPATDITDKMQTSLDEVMKTPKIIIGCFVAVTLAAAMLIVFYKLRKHQRQS  
 TVTAARTVEIIQVDEDI PAATSAATAAATPSGVSGE GAVLPTIADHINYNTRYKLRPHAGWTE  
 NSLGNLSLHPTVTTISEPYI IQTHTKDKVQETQI

[illegible]

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHFHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTCKKPALPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRS PGFKNDTLRSG  
VVSVDLSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMLGLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK

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ACCAAGGCATTTGTATCTTCTCAGTTGTGCATCAAGTTCGCAATCAGATTGGAAGAAAGCTCAACTTGA  
AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAACATGGGC  
TTCAACCTGACTTTCCACCTTTCTCACAATTCGATTACTGTTGCTGTTGACTTTGTGCCT  
GACAGTGGTTGGTGGGCCACCAAGTAACACTACTTCTGGGTGCCATTCAAGAGATTCTCTAAAG  
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAGAACTCTGACT  
AATGAAGCATCCACGAAGAAGGTAGAAGTTCGACAACTGTCTCTGTGTCTCCTTACCTCA  
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGGAAGAGGTACAGGCAGAAAAATC  
CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTTCGCCATC  
CTCGTTCCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAGAAAGT  
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATGGGAC  
TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAGGTGTGA  
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGTACAGGTTACGTTACAGTG  
GATATTTTGGGGTGTTACTGCCCTAAGCAGAGACAGCTTTTTCAAGGTGAATGGATTCTCT  
AACAACTACTGGGATGGGGAGGCGCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG  
AATGAAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
ACAAAGGCAATGAGGTGAACGCAAGACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG  
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
TATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGG  
AAGAACTGATTCTTTGTTTGCATAAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTCTTTTGTATTTTCTTAGCAGAGCT  
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG  
AGGGTTAAATATTGTAATATGGATACCTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT  
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT  
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCT  
GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCCACGAATCA  
GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGTGGAGTCTCGGCTGCAAAAGGCAG  
CAGTAGCTGAGCTGGTTCAGGAGTCTGATAGCCTTCAGGGAGGAGCTCGCCAGGTATGGCT  
TCCAGTGTAGTCCCAACAGAGAAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA  
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTACATATTAACATAATAATAATA  
TGCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA



**FIGURE 161**

MGFNLT FHL SYKFRLLLLLTCLTVVGWATS NYFVGAIQEIPKAKEFMANFHKTLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIKPDLTLEEVQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN  
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGVTALSREQFFKVN  
FSNNYWG WGGEDDRLRLRVELQRMKISRPLPEVGK YTMVFHTRDKGNEVNAERMKLLHQVSR  
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGAGGAGCGACCGCCGAGTTCTC  
 GAGCTCCAGTGCATTCCCTCCGCGTCCGCCACGCTTCTCCCGCTCCGGGCCCCGA**AATG**  
 GCCAGGCAAGTGTGGTCCGCGCTCGGCCGATCCTCTGGCTTGCCTGCCCTGCCCTGGG  
 CCGGAGGGGTGGCCGAGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA  
 CGGGAGCGGTGGTGACCATCTCGGCCAGCTTGTGGCCAAGGACACAGGCGAGCTGGCCCTG  
 CCGCTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA  
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCCGG  
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
 GTCTCTCCCATCACAGATTCTCGTGGGGACCTTGTGTACCCAGAACACTTCCCTACC  
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA  
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGAGCGGACCCAGATG  
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCAACGTGAAGCT  
 CAAAGTGGTGGCGGAGTGGGAAGAGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA  
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGG  
 CCCACCTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC  
 TCTGACTGTGTGCTGGCTCTCAAGCTGAGTGCCTCCCGCTGGAGGAAGGGGATGCCACC  
 CTGTGTCCGTGGCCAGCAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC  
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACATCAGTACCACAAGATCCAGGT  
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA  
 TGTGGCCCTTATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
 AACCCGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTGT  
 GGAGACTCCATCTGAGTACCTGGAAATGTTCGTGAGAACCAGGGCTGCTCCCGCCCTCT  
 ATAAGTCTGTCAAACTTACACCGT**GTGA**GCATCCCCCTCCCCAACCCATCTCAGTGTAA  
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTATT  
 TCGCTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTTACGCCACTGCCACAAGCC  
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA  
 TAAGCCCCATCCGGTTACACCCCCCTTGACCCCCATCTTTGAAGAGGCTTCGTGAGGACT  
 TTGATGCTTGGGGTGTTCGGTGTGACTCCTAGTGGGCTGGCTGCCACTGCCATGCCATTCCT  
 CTCATATTGGCACATCTGCTGTCCATTGGGGGTCTCAGTTTCTCCCCAGACGCCCTAC  
 CTGTGCCAGAGAGCTAGAAAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC  
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACA  
 CACACACACACAGAAATATAAACACATGCGTACATGGGCATTTTCAATGATCAGCTCTGTA  
 TCTGGTTAAGTCGGTGTGCTGGGATGCACCTGCCTAGAGCTAGAGCTCAAGAGGAAATTTGACCTCCA  
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTGC  
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGGACT  
 AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACTTATTTTATCGAAACCCATCTGTG  
 AAATTTTCACTGAGGAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGGCGGG  
 TGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCAGGCCGGTGGATCACAGATCAGGA  
 GATCGAGACCCCTGGGTAACACCGTGAAACCCCGTCTCTACTAAAAAATACAAAAGTT  
 AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
 GTGCCAACCCGGGAGGCGGAGCTTGCAGTGAGCCAGATGGGCCCATGCACTCCAGGCTGA  
 GTGACAGAGCGAGACTCTGTCTCCA

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**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF  
VVLPITEFLVGDVLTQNTSLPWSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCQCCGPFLETPSEYLEIVRENHGLLPPLYKSVKITYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT  
GGGCGGCTTGCCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA  
CAACAGACGGGACAAC TTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG  
CCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA  
TGGCTGGTTCTTTGTTTCCAAA  
AA

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**FIGURE 165**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCCHRSKCGMCKT

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CTGTGACGAAGGACCATCTGAAGGCTGCAATTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
CTGATATCTTCCACCA**ATG**CTTCTGTGTGTGCTTTTATAGATCGATTGTCAACCTTCTGGGC  
ATCTCCCTGACTGCTCTCTTCAACCTCCCTTCGTTTTCATATAGTGCACCACTTTTGG  
AGTCTCCTTTGGTATTCGCGAACTCTACATGAAAAGTCTGTTAAAAATCTTGCCTGGGTA  
CCTTGAGAAATGGAGCGAGGAGCCAAAGGAAGAACCACAGCTTTACAGCCCTACACAAC  
GGAATCAATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCGTGCAAGTGG  
TAGTAGTAAGGCTCTGCGAACCACTCCAGAGTTCGAGCTCTGACATTTTCTACTTTTGC  
GAAAGAGATAGGAGACATAATGAGTATGAGGTGACAAAGAGATTCCAGCAAGAAGATCG  
CAGTCTTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
GGTCTCTGTTGGGGTGGAGAGTGCTGATTCCGGTATGCTTCTGCTGCCCTCAGGATAGCAC  
TGGCTTTCACAGGGAATGAGCTTCTGTTGCTGGGCACAACCTGGTGGGATACTTGCCAAAT  
GGGAGGTTTAAAGGAATCATGATGAAACATGTTCCATGATTTAGTTGTTACCGGATCGCTGCG  
AGCGCTGACAGGCATCATCACTACCTACATGACGGAAACACAGCAAGAATGGTGGCATCT  
GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC  
ATGGTGGGTCAAGTGTACGCGGGGACATGTGGGTGTGATTCCAGAGAGCACTGGTGAAGGCGCT  
CCCCACAGCTGTGGTTGAGCGCTCGGAAGTGAAAGATGCCCACTGTGTGGCTAAGAGACTGA  
CTGAACATCTGCAAGATAAAAGCAAGCTGCCTATCTTCCATCTCCAGAAAGGAACCTGCATC  
AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGAGCCACAGTTTATCCC  
TGTTGCTATCAAGTATGACCCATAATTTGGCCGATGCCTTCTGGAAACAGCAGCAAAATACGGGA  
GGGTGACGCTACCTGCTGCGAATGATGACCAAGCTGGGCCATTTGCTGCAGCTGTGGTACCTG  
CTTCCCATGACTGAGGAGGCAGATGAAGATGCTCTCAGGTTTGCGAATAGGTTGAATCTGCG  
CATTGCCAGGCGAAGGAGCATTTGTGGACCTGCTGTGGGATGGGGGCTCGAAGGAGGAGAAGG  
TGAAGACACAGCTTCAAGGAGGAGCAGCAAGCTGTACAGCAAGATGATCGTGGGAACCAAC  
AAGGACAGGAGCGCCTCG**TGA**GCCTCGCTCCAGCTGGCTGGGGCCACCGTGGGGGTGCCAA  
CGGGCTCAGAGCTGGAGTTGCCCGCGCGCCGCCCACTGCTGTGCTTTTCCAGACTCCGGGT  
CTCCCCGGCTGCTCTGTGATCCCGAGCATCCGGCTTTTCCGCGAGCCGACGAGGGATCCCTGT  
GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGG  
CGAGATGCTCTGTTTCTTTTACAATAGTCTGTGGAGGAATGCCATTAAGTGAATCCCCCA  
CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGAGGATGTGCCATGTGCTTGTGCTAGAGAT  
GGCGGTGCAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTTGGGGGCGGCCACCCG  
CTCTCAGGAAGAAGCACAAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCCCCAGC  
CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCACTCTGCAGGGGCTTTTACGCAAAATG  
AAGGCTTAGATTTTATGCTGCTGCTGTGGGTTTACTAAAGGGAGGGGAAGAGGCGAGGTG  
GGCGCTGACTGGCGGCATGGGGAGAAGCTGTGTTCTGATCTCAGGCTTAACCTGAATCCCC  
ATGTGATGCGCGCTTTTGTGAATGTTGTCTCGGTTTCCCCATCTGTAATATGATGTGCGGGG  
GAATGGTGGTGATCTTCACTACAGAGGCGTGTGTGGGATTAAGATGCTGCGGGTGAGTGA  
AGGACACATCAGTTCAGTGTTCAGTATCAGGCGCCACAAAACGGGGCACCGGCGCCTGAG  
CTCAGAGCTGCTGCATCGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA  
TGA

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**FIGURE 167**

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELS DIFYFCRK GME  
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG  
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH  
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

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GCCCTCTGAAACCAGGACTCCAGCACCTCTGTTCCCGCCCTCACCCGGACCCCTGGCCCTCA  
 CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC  
 ACCTGGCAGGCCAGGCTGTTCCACCATCTGCCCTTGGGCTTGCTCCAGACACCTTTGA  
 CGATACTATGTGGGTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
 AAATGCCACCACATGCCCTGCTGCGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC  
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT  
 CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
 GCTCCCGGAGCTCTACATGAGGCACCTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG  
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
 TTGCCTCCAGCTCCCTGGATAAAGGCAGTGGCCCACAGATTGGGGAGAAGAGGCGGGGCTGT  
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTGCCCCCTG  
 GAAGACTCTGCTCTTGGCCCCTGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA  
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
 CAGCCTTGAGAAGCAAGAACTATGTTCCGGACCAGCCACTAGCAGCTTCTCCCCAACGAG  
 ATGTTGGCCTGGGAGGCCACGACGGCTGAGGAACTCTGCTATGTATGTATGGGACCTTCT  
 GGGACAAGCAAGGAAAGTACTGAGGCACCACTTGATTGAACGGTGTGCAATGTGGAGACA  
 TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA



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**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL  
YMRHFPPKALHFYLIRALQLLRSGGCSRGPGEVVRFGVGLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLAPGEFQLSGVGP

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**FIGURE 170**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACGAAGAAGATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTGTGTCTCCTGTTGGTGCCCCCT  
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCCAT  
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAATCCCCACTCAC  
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG  
CACTCCCTAAGTCTCTGCTCA

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**FIGURE 171**

MAGSPTCLTLIYLWLQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVS RNFS PILARKLCEGAADDPDSSMVLLCLLLVP LLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTYDTIPHTNRILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

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**FIGURE 172**

CTGGTTCCTCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCCGTGAAAGAGCTGGTTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAATGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGCTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCTCT  
GTGTCTCCTGTTGGTGCCCTCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAA  
AGATGGAATCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCCTATGAG  
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAATGAAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCTTGACAAT  
TTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLLCGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSDDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGCTATTGCT  
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAA





**FIGURE 177**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCTGGTGGAATTAGTGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTCAACGACACC  
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

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**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCTCTCCCCCTGCAGCCCTGCCCTC  
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG  
CCCCACCACCCCTCA

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**FIGURE 180**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK  
YKSSQKQHSPVPEKAIPILITPGSATTC

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**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCC  
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCC  
 AGTGTTCACACAGCCCCAAAACGGAACGTGGTTTGGGGTCACTGGGCCTGATCACTCCT  
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCAGGGCTTTACGGT  
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA  
 CCAATGCCTCAGTGCCTATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA  
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCTGAGCATGTTTGAG  
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
 TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA  
 GAAGCCAGCATATCCTCCAGCAGATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC  
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCTATCCGGGAGCGGCGTGG  
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGAGATGAGGAT  
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
 CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC  
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC  
 TTCCTGACCATGTGCGTGAAGGAGACCTGAGGTTACATCCCCAGCTCCCTTCATCTCCC  
 ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
 TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGTCTACGAC  
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC  
 CGCAGGGGCCAGGAAGTGCATCGGGCAGGCGTTCCCATGGCGGAGATGAAAGTGGTCTGG  
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA  
 TTGATCATGCGCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCA  
 GTGACTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITI FNKSANIMLDKWQHLASEGS  
SRLDMEFESISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDEG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLA RHPEYQERCQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWL RVEPLNVGLQ

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**FIGURE 183**

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC  
AGTGTGGAGAAAACTAGGCAAACCTACACCCTGTTTCATTGTTACCTGGAAATAAATCCTCT  
ATGTTTTGCACAAAAAAAAAAAAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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**FIGURE 185**

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAAGTGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGCGAATAAATGTTCAAAGTGA

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**FIGURE 186**

MPSPGTVCSELLLGLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGGTGCTGT  
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG  
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT  
 GTCCCCCGTGTGCGCATGTGTTCAAGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAAA  
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
 TCAGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTACA  
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
 CCAAAAACACAAGTAGAAATTTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA  
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT  
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC  
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGCCCA  
 ACCCTGGTCAGGGCAGAGGGAGTTGGTGGGTGAGCTCTGGGCTCACCTCCATCTCCAGA  
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACAAGA  
 GCCTCCTTGTTTCATAACACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT  
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA  
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 188**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLFLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW  
VVRAAHLTPLEIVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAEELTPRPAGVVPGA

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**FIGURE 189**

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG  
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAAGTGCTTTGACATGCCAGTGTCCCTG  
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA  
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG  
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA  
 GGACTACTGGAATTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA  
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCTCCCTTGGGGCTTTGTGGCAAAATCCTA  
 TGGTTATCCTTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCCTCCTGCT  
 ACTAACAGACTTGCTACTCAGTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGTGTG  
 CTGTTTCCTCTGTCTGTCTGCTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC  
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGGCTG  
 GGCTTCTACATGGCCTGGCTCTCCTTACCTGCTGCATGGCGTGGGCTGTACCACCTTCA  
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAC  
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC  
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCATCCACTCTGTCTCTGAGG  
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTTGGGGA  
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
 CTAAGGGATTCTTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCAC  
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTSTQEVVQYNWETGDDRFSSFRSFGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCCAGATGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCCTATTCTGTCACTTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCTATTCTCTCTCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCGTAGATTAG  
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTCCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT  
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA  
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTATCGGAAAGATCATCCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGATTACCTGCTGG  
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAATTTCTTAACACTGAAA

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**FIGURE 192**

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGSGME  
HRNHLCFCDLYDRATSPPLKCSLL

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**FIGURE 193**

GTAGCGGCTCTGGGCTCCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCTGGAGCCAGGAGCGACGTCA  
 CCGCCATGCGAGGCATCAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGTATGCTT  
 GGATGTGCCCTTCCAATATACACAAATACTGGCCCTTTGTCTATTTTACATCCTTTCACTTATTC  
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGAAGGAACCTGCCATCTTTC  
 TTACAACGGGCACTGTCTGTGAGCTTTGGACTCCCTATTGTATTGCGAGAGCACATCTGATTGAGTGGGA  
 GCTTGTGCACTTCTCTCACAGAAACACAGCTATCTTTGCAACTATACTAGGCTTTTGTCTGTCTTTGGAAG  
 CAATGACGACTTCAGCTGGCAGCAGTGC~~TGA~~AAAGAAATTACTGAACTATTGCTCAATAGGACTTCCGTGCTATT  
 GTTGGCCATTACGCGACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTGGGGGTATTTTA  
 GGTGCTCCCTCTCAGTTTTATTGTAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTTAAAGGATTTTCT  
 CTTTGGAAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTCTGCAATTTAAATAT  
 TTATGTGTTTTCTGTAGGTGATTTTTTGGGAATCAATAGCAATGTTAAACACTTTTTATGTATATCA  
 TTTGCATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTCTCTAAATATAT  
 TAGCCTCCATTATTACAAAAAATTATAAAAAATAGTTTTCACTGAGTCAAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTATACCTCAGAG  
 GGGCCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATATTTTTATGGAATTGCTACAGAGGAGTGCTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA  
 AGGTAAAGGGTGTAAAAACATTTTGAGATAAGGTTTTATTATGTTTATTATTTGTTAGAGTGAAGTGAAGT  
 GGGAGAAGATGACATTGAAATCCAGTTTTTGAATCCTGTTCTATTATTAAGTGAAATTTGTGATCTCCTATC  
 AACCTTTCATGTTTTACCTGTTAAAAATGGACATACATGGAACCACTACTGATGAGGGACAGTGTATGTTTGC  
 ATCATATATGCCAGAAAACCTTCCCTGCTTCTCCTTTGACTTATTGGTATGTTGTATATATTACATAAAA  
 TAACTTTCAAATATAGTTTAAATAACACTAGAAAGTGTACTTACCTGGAAAAATATGCTATGCCGACATT  
 CAGAGTGCCCTCCCTGCAAGGCCCTGGCCATGATTAACAAAGTAACTGTTAGTCTTACAGATAATTCATGCA  
 TTAACAGTTTAAGATTTAGACCATGGTAATAGTAGTCTTATTCTCTAAGTTATATCATATGATTTAAAAAG  
 ACTTTAAAGCAAGTTTCTGTATACCTCTGAACTGTTTGGATTGAGTTTCAATCATGATAGATCTCTGTTTT  
 CCTTTAAAGCAAGTTTGTGTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAATTCAGATAGCCAGGATGATCAATTTATAGTGGTGGTTTACATCTAATAATTTACAGGA  
 TTTTATTCAGGAGTGGGTATAAAAACATTCAGTTGGTCTGACAGTATTTGTTAAGGATATTTGTTGTATG  
 TTTATTCAGTATACCTTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
 TTTATGAAGTTATTTCTCAAGAAATGGGAATAAATTTGGGATTTGTTGAGCTTTTTTACTAAAGATGCCATAA  
 AGCCACAGGTTTTATTGCCCTAACTTAAGCCATGACTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG  
 CGGTGTGCCCTGGAGCCTTCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTGAGATTTCAAGAGGAA  
 GGTGACAGGTACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTGTGATCTACTGGACTTT  
 TTTTTGCGAGGAAGTGCATCTCTGCTCTCCCTATTTTCTGTTCTGGATGTCACTGCACTGCTACTG  
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATCAATTTGATTTGGCAGATT  
 GTGCTTTGACCTTGATACTAGCTGTGATAGTGTCTCTGATTCTAGGCTAGTACTTGAATATGAAT  
 TTTCCATAGAATATGCACTGATACACATTACCATTTCTCTATGGAAGAAACCTTTTGTATGATGAACAATAA  
 AGATTTTAAATATCTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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[illegible]

**FIGURE 196**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNHICSVQGDADFQKLRRVKELTLSSNQ  
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVVRIFQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLHSLCLRNRKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSITSIT  
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCSCHQQPARECEV

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**FIGURE 197**

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA  
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGGCCGTTGAGTTCCCGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCTGGCTTCAGGAGCCGGATTCCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC  
CACGACGACGTCTTCTTCCGCCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTCCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTTGGCGTCCCGCGGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCCTG  
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCT

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**FIGURE 198**

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE  
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA  
PGLFFVDAERVPCRHDDVFFPPSASFVGLGPGASPVVRVRSISALGRFTTRDEDLAVFLASR  
AGRLRFHGPALSVGPEDCADPSGVCVCGNAEAQPWICAALLQP

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**FIGURE 199**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT  
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT  
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACCTTATCTTCTGCATTTTGCAGTCTTTGGCA  
TTGACGTGGTACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGC  
CGTGTGTCTTGCATTAATTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG  
CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT  
TGCAGCAATGTGTTGCTTGTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT  
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA  
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAC  
CTATTGAGCAACAGCAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP  
FARDAVKKCFVCLA

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CTGAGGCGAGTGTACTCTGGCGCGTCTCGGCGGCGCTTCTCCAGTCAACCCTCCGCGCGTCTCTCCGCGGCGCGCG  
CGCGGAGGACTCGTCTCCAGACCTCCCTCCCGTTCTCCAAATAATACGAGTACAGGAGATCGCTCGAGGGT  
GGGAGAGAAATTTAGGCGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATATCTTACACTG  
AACTGATCAAGTACTTTGAAATGATCGATTCCGAATTTATCTTGGTGCTCTTCAATCTGCTGCACGTGCTTTC  
AACCCCTTTTCTCTCCAATCAGGACAGGCAAAAGGTTCTACTAGTTTCTTTGATGGAATCCGTTGGGATTACT  
TATATAAGGTTCCAAAGCCGCCATTTTATTATATATTAAGAATATGGTGTTCACTGCGAAGCAAGTTACTAATGT  
TTTATTACAAAACCTCACTAACCAATATATTGGTAACTGGCCGTTCTTCAGAGAATCATAGGGAATGTGTG  
AAGATGATATGTTTGACTCTTATCGGAACAAATCTTCTCTCGGTGATACATGAATATTTATGATTCOAAGTTT  
GGGAGAGAGGACACCAATATGGATCAAAACGAGGAGCCAGCATAGTGTGGCAGCACTGTGGCGCGGA  
ACAGATGTAAAAATATCAATAGGCGTTTCTCTACTCATTAATGCCTTCAATGATCAGGATTTCAATTGAAGATAG  
AGTTGCCAAATTTGTTGAATGTTTACGTCAAAAGAGCCCAATCTTGGTCTTCTCTATTTGGGAAGACCGTGT  
ATGACATGGGCCCAAGTCTGGGACGCTGACGTCGCGTCACTGGGCGCTGTCAATTCAGATATTCAGCAAGAAGTTA  
GGATATCTCATACAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTTAATCATCAGACGATCATGG  
AATGACGCGAGTGCCTGTGAGGAAGGTTTAATAGAATCTGACAGTACATCTGGATAAAGACAGATTAACCGTGATTG  
ATCAATCTCCAGTAGACGCCACTTCCGCAAAAGAAAGTTGAATGATGAGTCTATGAAGCACTAACTCAAGCT  
CATCTCTAATCTTACTGTTTACAAAAGAAAGACGTTTCAGAAAGGTGGCATTAACAATACACAGCTCGAATTTCA  
ACCAATCATAGCAAGTGGCTGATGAAGGTTGGCACATTTTACAGATAGTTCAGATGACTTCTGTGGAGCAACC  
ACGGTTACGATAAATCGGTTAGCAGATATGCATCCAAATTTTACGCCACTGGTCTCGCCTTCAGAAAGAAATTTCA  
CAAAAGAGCAATGAATCCACGATTTTATGCCACTACTATGCCACCTCTCAATATCACTGCGCTGCCACA  
CAATGGATCACTTGGAAATCTCCAGATCTGCTCAATTCAAGCAATGCCAAGGTCGTCCCTTACAGACAGCTA  
CTATCTCTCCTCCCTGTTAGTGTTAACACGAGAAATGACAGAGGCTCATACCTTTATTCATAGGGGCT  
TCTCTTGGCAGCATATATAGTGAATGTATTTTGTGAATTTTCAATGAAGGTTTAATTCACAGTCAAAATCACTGCT  
CTTACAAGATATGCATCGTGAATAGCTCAACCAATATTACAAGCGTAAATGTACTTGAAGTGGAATTTGCATA  
TTGAAGTGGAGATCCATAAATATGTGCACTGTTTAAAGGTTTCAAAATCTGGGAAGACAGTTCCAAACATCTGT  
AGAAATCAATTAAGCACTACATATTTAGGATATACACACACACACACACACATACATACACACACGCGGCAAA  
ATATCTTACACCTCGAAAGGAATAAAGATGTGAGAGATGTCTCATTTGTTCACTGTAGCATAGGATAGATAG  
ATCTCGCTGTTTATTTGGACTTGGCGCAGATATGTATATATTTTGGCACTTTGCACTATGTAAAGTACTTATAT  
ATTGCACTTTAAATTTCTCTCTGTGTGATGGGTATTTTAAATTTGAAATGCACTTTATGACAGATTTATGTCTTATAAC  
TTGATTGAAATGACAACTTTTGACACCAATGTGCAGAGATACCTTTGTACGATTGTCTTCAACTGAAGGAAT  
TCTATAAATCCGGAATTAATGAACATAGAATATCTATCCATAATGAGAGAAGAAAGAGTGATAAGTGTGGA  
AAATTAATGTGATAACCTTGAACCTTGAAATTTGGAGATGTTTCCCAACAGAGATGCAACTGTGGGCACT  
TCTCTGTCTTAATTTCTTTCAGAGACAGCTGGTTTCAATTTATTTTCCCTCCAAAGACAGATCAAAATACGTGACAG  
ATTCTGCTTCAAAATATTTGTTCTGTCTCATAAAATTTATGTGATTTCCGTGATGATCAATTTACTGTGATTTTCA  
TAATATGAAGGACACCATGAATATCTTTTCTCTATATTTAGCAAAATGGCCTGAATAGAGAGACACAGGCA  
CAACTCTCAGCAATGTTTCTCTCTTTGTTAAATTTATGTCCTCTTGAAAATTAATCACTATTAAATCAATTAA  
CAATCAAATTTGGATAAAAAAGAAAAA

**FIGURE 202**

MTSKFILVSVFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW  
 ITNQAGHTSGAAMWPGTDVVKIHKRFPTHYPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER  
 LIELDQYLDKDHYTELIDQSPVAAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
 SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCAG  
GACAGGCCACCCTGCGGGGCGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCCTTGCTTGGGTTCACACAGCCAAGGAGGCAGAGCCAGAATCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCGTGGGAGACGA  
CTACCATGCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG  
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCGACGTTGCC  
CCTGCCCCGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTCTCGGATGCCCTCCTGGTGC  
TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG  
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCCGTCGTGGTGG  
TGGTCTCATTTCATCTGGACATTGTCTCTGTTCCAGGAGCACCAAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGTGTCTGAGAAGCCCCGAGCTGATGAGTTTGCTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCAGTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCTGTTTTCAATCACAGAGAACAAAACC  
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGACAAATAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERMASKFLRHFTTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELIDL  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS  
CSEKPLD

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CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCCAAT**TG**  
**G**CTCTGTCTTGCTGCTGTACGTGTGCGCGGTCTCGGGGAAGCCCGACAGCGAGTTCCAGTACTTTTG  
 AGTCGAGAAGGGGCTCCCTCGCGAGCTGAAGTTCATATTTTCAAGCTCAGTGTCTTCAITCCCCCTCC  
 CAGGAATATCTCCACCTACCCGCAAGTGGAGCGAGAAAAATGTACAAGCTGGAGATAAAGACCT  
 TGAATGGGCAGCTAGACTTTGAAGAATTTTGTCTATTATCTCCAAGATCATGTGACGAGATCGA  
 GCGTGGTGTGTTTAAAGATTTTGGACAAAAAGAAATGATGGACCGATTGACGAGCAGGAGATCAT  
 CAGTCCCTGTCGGGAGCTGGGAAGTCAAGATATCTGAACGACGAGCAGAAAAAATCTCAAGAG  
 CATGGATAAAAAAGCCGACGATGACCATCGACTCGAACGAGCTGGAGAGACATCTACCTCTCTCC  
 ACCCCGTGGAAAAACATCCCGAGATCATCTCTACTGGAAGCATCTCCACGATCTTGAATGTG  
 GAGCGAATATTAACGGTTCGGGATGAGTTTACAGTGGAGGAGAGGCACGCGGATGTGTT  
 GAGACACCTTGGTGGCAGGAGGTGGGGCGAGGGCGGTATCTCAGAACCTTCAAGTCCCGGCTG  
 ACAGGCTCAGGTTGCTCATCGACAGTCCATGCCCTCCCGCAGCAACACATGGCATCTCTGGT  
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGAGAGATCAAGCCGCT  
 CGTCTCAAAAATTGGCCCCGAATACGCCATCAAAATCATGGCTTGTGCGAGGCTCTTGGA  
 TTGTTGGTAGTACCAAGGAGACTCTGAGGATCTACAGAGAGCTTGTGCGAGGCTCTTGGA  
 GGGGCGACTCGCCAGAGCGAGCTCTACCCCAATGGAGGCTCTGAAGACCCGATGGCGCTCGG  
 GAAGACAGGCGAGTACTCAGGAATCTGTGAATCTGAGGCGAGGCGGATCTGGCCAGAGAGGGG  
 TGGCCGCTCTTCAACAAGGCTATGTGCCCAATATCTGAGTATCAATCCCTATGCGCGCATCT  
 GACTCTGCGATCTACGACAGCTCAAGAATGTGCGCTGCACACTATGCAATGAACAGCGCT  
 GGACCCCGGCGCTGTGTTGTCTGTGGCGTGGGACATGCGGACATGCTGCGCCAGCTTGG  
 CCAGCTACCCCTTGGCCCTAGTCTGGACCGCGGATGACCGCCAGGCTCTATTGAGGGGCGCT  
 CCGGAGGCTGACCATGACGAGCTCTGAACCAATCTCTCGGACCGAGGGGCCCTTGGGCT  
 GTACAGGGGGCTGGCCGCAACTCTCATGAAGTCACTCCAGCTGTGAGCATACGTCACGTGTC  
 TCTACGAGAACCTGAAGATACCTTGGGCTGCACTCGCGGT**GA**CGGGGGAGGCGGCCGCGG  
 CGAGTGGACTCGCTGATCTGGGCGCAGCTGTGGGTGTGCAACCATCTATTTCTGTGAATG  
 TGCCACACATAGCTGTCTGCAAGTCTGCAAGTCTGCAAAACCTAGACGACCCCGAGGAGGGT  
 GGGGAGAGCTCGGAGGCTGAGGCTCTGCTCTGCTACCCCGACGACACCCCTCTGTGTTGTT  
 AGCGAAGACACAGGATCTCTGATAGCTCAGGGTCAGCAGGCTCCGGGCTCATGTGTGTA  
 GGACAGGACATATTTCTGATGCTGCCATTAATGATGAGCTTGGACCTTGGAGCGCGCTTAGT  
 TTGTCATTTCTGCTTCCCTTGCACTGCACTGTGGCCAGCGCCCTGCCCTCTGTCTGCCGTG  
 ATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGTGAGTAAAGTTGGGAGGAGGCTACAG  
 CCAACATGACACCTCTGCTCAATCCCAATATCATGAAAGTGAAGTCACTGCTGGCTCT  
 CACCTGCGTCACTTCCCAACTACAGCATGACGCCCACTTGGCTGTGAAGGAAGGAAGAA  
 GATCTGGCTTGTGTTCACTGTCATCTGAGCTGATGGCTGGGGCTCTCGGGATGCT  
 TGGGATGCAAGGCGGCTCGGCTGCTGCTGGCTGGCTGCACAGAAGCAAGTGTGGGGCTCA  
 TGGTCTCTGAGCTGGCTGGCTGGACCTCTCAGGATGGGCCCACTCAGAACCAACTCACTG  
 TCCCCTCTTGCCATGAGGCAAGTGGACACCATGTTGAGGGCAGAAGGCGAGCTTTTG  
 GTGTTCTGGGAGGGAAGAAAGTGTGAGGCGCTTAATTTGAGCTGTGTGGGAAGAGGG  
 TTTTCTCCAAGAGCAACGCGGACAAATGAGCACTTCTGTGCTCCAGAGGAAGCAGGAGG  
 GAGCAGGAGCTTGCTGCTACTGCTCAGAGTCTGTTCTGAGCCCTGGGGGTTCCGTGTCAACC  
 CCAGACAGGGGCGAGCGGGAGCGGCCCAATTCACATCTGTGCTCACTGCTTGGAACTTAATT  
 ATTTTGAATTTATTTGAACAGAGTTATGCTCAATATTTTATAGATTTGTTTATTAATTA  
 GCTTTGTCATTTTCAAGTTATCTTTTTTATCATATTTATGTTTCATGGTTGATGTGATCTCCC  
 AGACCCGCGCAGTGGGATGGGAGGAGGAGGAAGGGGGGCTTGGGCGCTGTCAGTTCACAT  
 CTCTGCCAGAAAAATTCCTTTGGGACTGGAGCGAGAAAAGCGGCCAGAGAGGCGAGCCCTG  
 GCTCTTCTCTTGGCAGGTTGGGAAGGCTTGCCCCAGCTTAGAGTTACAGGTTTGA  
 CTGGGGGGCTGGAGAGAGAGGAGGAACCTCAATAACCTTGAAGGTGGAATCAGGTTATTTCT  
 CTGCTCTGGCAGGTTTCTTTATTTTACTCTTTCTGTAATGCAAGGCACTGAGGTGCTCT  
 CACTGTGAATTTGCTTGGCTGGCGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCGCTCTCC  
 CAGCCTTCTGCTGGCTTGCTTTAACATCGCGGCAACTGGGCACCTACGGTGTGCACTTCTG  
 ATTCACACGAATGACCTGATGAGGAATCTCAATAGGATGAAGAATCAATGCAAAATTT  
 GTTATATTAACATATAACTGGAGTCGTCAAAAAGCAAAATGAAGAAGAAATGGACGCTTAG  
 AAGTTGTCAATTAAGCAGCCTCTCAATAAAGTTGTTTCAAGCTGAIAAAAAAAAAAAAAAA  
 AA

**FIGURE 206**

MLCLCLYVPVIGEAQTEFYFESKGLPAELKSIFKLSVFI PSQEFSTYRQWKQKIVQAGDKD  
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKN DGRIDAQEIMQSLRDLGVKISEQQAEKILK  
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
 WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI  
 NVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAI AQSS IYPMEVLKTRMAL  
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS  
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSSLFKHILRTEGAFG  
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

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**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT  
GGCTTCCCTGGGCGAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG  
 CAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA  
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTACAGAGCCCGACAGCAGTGTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGTTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA  
 TGAAGGTTGTGCTGTGCTCTACAATGTTACGATCAACAACATACTCCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTTCTTTCTTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA  
 AGAAACAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA  
 GACATATTAGAAGTTGGGAAAATAATTCAATGTGAAGTACACAAGTGTTAAAGAGTGATAAG  
 TAAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT  
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA  
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT  
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGACACCGATTTTATAATAAACTGAGCACCTTCTTTTTTAACAAAAAA  
 AA

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**FIGURE 208**

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD  
AGTYKCYIIITSKGGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

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[illegible]

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPF  
LNQCGSLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRRLDYCECGTQLCGS  
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVFFPWTVWRKTEAGVWD

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CTTCTGTAGGACAGTCCACGAGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT  
TTGCCAGTGGGAAGTACCTAGTGAACGCGCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCA**ATGA**AGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGTCTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCAGTGTC  
GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGTCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCTTCCCCTGAAGAAGCTGTCCAGCAACGCAGAGTGCCCTGCTTGTATTG  
AATCTAATGGAACCTCCTGTCTGTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTCT  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC  
CAACGTCACTAAGCCACCTGTCACTTCCGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCA**AAATGTAA**ACAGCTTAACCCCCACGTCTGCACCAACCACT  
TCCCACAACGTGGGCTCCAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG  
GGGACTGCTGCC**CTGA**GGTCTTGGGGCTGCACCTTGGCCAGCACCCCACTTCTGCTTCTCTG  
AGGCTCAGAGCACCCCTGCGGTGCTGCACACCTCTTTCCTGCTCTGCCCGCTTAACTFCG  
CCAGTAAGTGGGAGTCAAGCTCTCCAGGCAATGCCAGACAGTGCCTTGTCTTCAATTATTA  
AAGCACTGTTTCACTTCACTGCCAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 212**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASIECPSHANTSCISSSASSSLETPVR  
LYQNMFCSAENCSEETHITAFTVHVSAAEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK  
TLGGVIFRKFEKANVNSLTPTSAPTTSNVGSKASLYLLALASLLLRGLLP

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**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCAAGGTAGGAGGCA  
 GGGCTTGCCTCACTGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG  
 GCGCGCTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGCGGGGGCCCAAGGCCTG  
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGGCCCATGACCCGCAG  
 CTACCGGAGCACGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC  
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGACTTCCAGTGCAGCTCCCA  
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
 ACTTCAAGCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG  
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC  
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT  
 TCAGTGTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC  
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG  
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA  
 GGATTGGCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTCACAGAGATGCAACCAATA  
 GACAGAAACCAGAGGTAATGGCCACTTCATCCATAGAGGATGTCAATATCTCAACCTCT  
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTACAGAAAAACAAACTGGAAAA  
 CACAA

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 11901

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**FIGURE 214**

MVPAAGALLWVLLLNLPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQQPCNRLREECPLDTSLCTDTNCASQSTTSTRTTTTTFFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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CCGGGCTCGACCCACGGCTCGGGGAGAAAGCTGGCGCTGGCGCGCGTGTGGTCTCTGAGTCTGGGGCA  
CGCGCGCTGCGGACGGCGCTCCAGGGACAGCTGAGCGAGCTACGCGCATCGGTATCTCAGTGCAGGAAGACA  
GAACCTGCTCTGGGGGCGCTGTAAATCACTCCGCTCCCGCCAGCAATATCATATGAGTCTAGCAGGCTGGACCT  
CTCGGGACGATCTTAAGTATGAGTGTATGGGTCACCTTGGGCTTACCTCCAGAAGTCTACAAAGTGCT  
CAGTCTGATGCAAGTGGCCCTCTCCCGGTTCTGTTCTTCAGAGCGGGCATCGGCGCTGGCTCGTTTCT  
CAATGGCTGGCCAGCTGGTATGATCTCGGCTCGCCGACCTTCGTGGAGCGCTCTCCCCATGTACCACTA  
CTGTGTGGGCTCTGGCTGGGTGGCTTCAATCATGGTGGTTGTGTCACAGATCTCCACACAGGACATGA  
CTCAGAGAGAAATGGAATCACTTCTGTGCTCCACTGTACTCATCACTCAATCTCACTCTGCTCGAGG  
CTGGGGGCTCGAGCACCCAGCTGGGTGAGCTCTCCGGGGCTCTCTGCTGCTATGCTGACCGCTGACGCT  
CTTCACTGAGCTCACTCGCTTCGATATGGTCACTCACTGTGGGACAGCTGGCTATTTGGCTTGGTCAAGTGT  
GTGTGTGGTGGGCTGGTGTCTGTGAAACAGCGGGCGGTGCTCACTGTCGCAAGTGTGGTGGTGGTGT  
GTGCTGTCAGAGGGCTGTCTCTGCTCGAGCTGTTGATCTTCCAGCGCTCTTGTGGGTCTGGATGGCCATGCCA  
TTGGGCATATCAGACCATCCGTGTCCAGTCTCTTTTCCAGCTTCTGGAAGATGACAGCTGTAACTGTG  
AAGAAATCAGAGGACAAGTTCAAGTGGACTGAAGAGACTTGGAGCGACTGTGCCCGAGTGGGATCTGCCGCC  
GCCCTGTGGCTCTCCCTTCTCCCTTCAACCTCTGAGATGATTTCTTTTCAACTTTGAATCTGGACATGA  
AGGATGTGGGCGCAAGATCATGTGCGAGCCGCCCTCTTGTGGCGCTCACCAAGCTTGGAGTCTGTCTTAGG  
AAGGCTCCCGACATCTGGAGCTCGAGATGGGACGCCCTCTACTCTGGAGCTGAAATGGGGTGGAACTGA  
GTGTGTTTATGCTCTCAGCGGAGGAGACGTGCTGTTTCTCCCGACAGCGCTCTCTCCCACTATCCAGCTGT  
CTGTGCTGGGCTGCTGAAGCCCTCTGTCTATCTGGGAGACAGGAGACACAGCGCTTAGGATACAGGGGGTCCC  
CTTCTGTACACAGCCGCCCTCTCCAGGACACCACTAGTGGTGTCTGGATGTGTTTCTTTGGCGGACCA  
GTTTCAAGCGGCTTCTCCCATGGGATCTTGAGGAGCAAGCTCTGGGATGGGAGAGGATTTTCACTTGACC  
GTGTGCTTACGACAGGTTCCAGGAGGCTCTCACATCTCTCCCTTCAGGGCGAGGCTCCAGCAAGCCCGAGGCA  
AGGATCTGTGTGCTGTGTGTGTGAGAGCTTGCCACGCTGTCTGGGAGTGTGGGCGAGGCTGAGTGCATAG  
TGACAGGCGCTTGAGATGGGCTGGGTGTGTGTGATGCTCAGGCTAGGTCGAGCTGTGGAGACGGGTGTGT  
CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTCAGGGGGTGGGTGTGTGATAGCTGGGTAGGGGAAGTGT  
TGCCTGTGCTGGTGGGAGGCTGAGATGAGTGAAGCCGGTGAATGTGTCCACAGTGTAGAGGTTGGAGCAGGAT  
GAGGGAATCTGTCAACATCAATTAATCACTGTGGAGCGAGGCTGTCGCCAAGACGCCACTGGGCGGACGAC  
CAGGAGCTCTCATGGCGAGGCTGCTGTGTGATGTCTCCTGTGTGGCTCTTGGCCGCTCTCTCGCAAC  
CTACAGGGTCCCAACACACAGAGCTGCCCTCGAGAAGCAGCCCTCGGAGGACAGGAAGAAAATGGGATGGC  
TGGGGCTCTCTTCATCTCTCTTCTCTCTGCTTCGCTATGGCTGGCTCTCCCTCCAAAGCTCTTCATTCCTCT  
GCTGCGAGCCCTTTGGCATAGCTGATTTTGGGAGGAGGAAGGGGCGATTTAGGGAAGAGGGGAAGAAAGT  
TATGGCTGGGTGTGGTTTCTCTCTCTCCAGAGAGGCTTACTGTTCTCAAGGTGGCCAGGCGAGGGGCG  
ACATATGCTGTGGCTCGCTGTAAAGTGACCCCTGCATTTACAGAGCCCTGGCATGTCTCTGCCACAGG  
AATAGATGGGAGGAGCTCGAAACCTTTTCATCCCAAAAGGCAGTCTCGCTGGTTTGAAGCAGCATGTTATTTG  
CTGTGCCCTACCCCTTGCCTCTTTGAGGAGGAGGAGTATGTAAGTACCAACTCAGGAGCTCGGGTGT  
GCTTGGCTAGCTCTTTTGATATGAAACTTTTAAGTGGGAGGGTGCAAGGGATGTGCTTAATAAATCAA  
TTCCAGAGCTCAAAAAAATAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREFVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCR  
YRTFVPASSPMYHTCVAFAWVSLNAWFSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL  
KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

216/330, 216/330



**FIGURE 217**

GGCCGCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGAGGCCGAAGGTCCGTGA  
 CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG  
 CTGATGGCGCCTGTCTTACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC  
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC  
 TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG  
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGAAAAGAGAGGCCAA  
 ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCAAAGGCTGGATATCAACACCA  
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGCGCAGAGATG  
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA  
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCAATTGAGACTGACATGCAGATCATGG  
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC  
 TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG  
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGT  
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGA  
 GCCCTGCAGAAGCTGCTGGTCATCTTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT  
 CCTGTTTGCCTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCTTGAAGC  
 TCGGGGGGCTGCAGGTCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG  
 CGCTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTCGCCGAGGAGGAGGCTGA  
 GCTGACCCAGGAGATGTCCCGAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG  
 GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT  
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG  
 TCAGGACCCCGAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA  
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC  
 AGCTTGCTGAAGGAGCTGAGATTGAAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA  
 GGCTGAGGGGTGCCAGCGTGGTGGGCTTCTCAGGCAGGAGACATCTTGGCAGTGCTGGCT  
 TGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

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**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPKESSSTKETERKETKAEEL  
DAEVLVHFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDFRNNLKGKRLDINTN  
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIELKKDFDELNVVIETDMQIMV  
RLINKFNSSSSSLEEKIAALFDLEYVHQMNAQDLLSFGGLQVINGLNSTEPLVKEYAAF  
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
GGLQVRLTLVQEGTEVLAVRVKLLYDLVTEKMFEEEEAELTQEMSFEKLQQYRQVHLLPG  
LWEQGWCEITAHLLALPEHDAREVTLQTLGVLLTTCRDYRQDPQLGRTLGLQAEYQVLAS  
LELDGEDAGYFOELLGSVNSLLKELR

Important features:

Signal peptide:

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCC  
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTGCAGTGGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCGTGTCTGTGTCAGGCCCCCACC  
 TTCCCACTTGACAGCCATGGGGGGTGGGGTGTTCGGGTGCACTTTCGTGCGCTTCGGC  
 CCGGCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGT  
 CGCAGGGGCAATTTTCTGGCTGGTCTCCCTGCTCCTGGGCTCTGTGGTCTGGTTCATCTTGG  
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGGCTCCTGATTTTGGTGTGCT  
 GTCTGTGCTCTTACAGGAGGTGTTCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCT  
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTCTCTGTTATCAATATTTGGCT  
 GATGCACTTGGGCGAGGTGTGGTGGGATCCATGGGAGTACCCATTTACTTCTGACTTC  
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTGGGAGTACCTACTGACATCG  
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCAGCC  
 TCTTGTTGAAGGACTGACTACCTGGACTGATCGCCTGACAGATCCCACTGCCTGTCCACTG  
 CCCATGACTGAGCCAGCCAGCCCGGGTCCATTGCCACATTTCTCTCTCTCTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTGTCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCTGGGTTTCAAGCAGTCACTGAGTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCGCTGTGTGCTGCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGCCGACGCGCAGGAGCAGTCCGGTGAT  
 GGTGTATTTGCCCCTGCGCATCCCAACCGAGGACTGAGGGAACTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACG  
 GTTGCCAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC  
 AGGCCTGAGGGGGAAACCAATTTTGGTGTGATAAATACCCCTAACTGCCTTTTTTCTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATTTGAACCTCTTAACCTCCTTGGGCTATATTTCTC  
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTTCGGTCCCTTTTCTCCTTGGTCCAGACCT  
 GGGGGAAAGGAAGGAAGTGATGTTTGGGAACCTGGCATTACTGGAACCTAATGGTTTAACT  
 CCTTAACACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAAGTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTGCAGTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGGCGGGGAGGTTTCTATAAACTGT  
 ATCATTTTCTGCTGAGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTGACT  
 AATAAAAAAGAAATTTGTAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 220**

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVGIGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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**FIGURE 221**

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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**FIGURE 222**

GACCGACCGTTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCCTATTAATTCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA  
GAGGAG

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**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC  
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTCGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCTGATGCACCTG  
GGCCAGGTGTGGTTGGGATCCATGGGACTCACCC

**FIGURE 224**

GTAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTTCCCNNTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCCCTCCCATTGCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGTTTCGGGCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGCAGGGGC  
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA  
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTATCAATATTTTGGCTGATGCACIT  
GGCCAGGTGTGGTGGGATCCATGGAGAC

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**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC  
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG  
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT  
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG  
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCTTGGCTACTCCACCTTGGCCACTCT  
 AACGACCTCATGCTCATAACTGAACAGAAGAAATTCGTCCCCTAAAGATGTGAGCCCAT  
 CAACGTCTCCTCTCATTTGTCCTCTGTGGGACAAAGTGCTTGGTGTCTGGGTGGGGGACAA  
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGACTCGTGTCTGGGGAGATTACCTTTGTGCCGCCCAACAGACCGGGTGTCTAC  
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCTTGAGTCAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG  
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG  
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTCAT  
 CCTCAAGCTCAGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA  
 CTGAGAAGTGAAAAAAA

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**FIGURE 226**

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGR DSCQGD SGGP  
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 227**

**ATG**GTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA  
 CAAGCCGACGAGCCGCGAGCTCGGGTACGTGCTGTGCACCTGCTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGTAGCTGTCAACGGTGCCGTGCTCTTCTGAACCAACGCGCCACGGCCGCGGCACG  
 GCGCCCCACCTGTGCTCAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGGA  
 AAGGGCGGACAGCTCGCACTCAGCATCCTCATTGACCCGCGCTGCCCGACCTCAACGACA  
 CTTTCGCACGCTTGAGAGAGCGCCAGGCCCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC  
 CAGCGCAGCGCTGCTGGGCGACGAGCAGGAGCTGCTGGACAGCTGGCCGACCACTGCC  
 CGGGCTGCTGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGCGACGGCCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC  
 TCTGAGAGCGAGGCCACATGCTCACCCTGGTGAACCTCCCTCAGCGCATCCTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGCGCGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC  
 GGGGAACCGCGCCCGGGGGCTGTGCCACTGGCTCCCCGGCCCCGAGACTGCTGGAGCTCCTC  
 CTAAGCGGACAGGAGCATGGGCTCTACTCTGCTTTCCCAACCACTACCGGGCGGGCTT  
 CGAGGTGATCTGTACATTCGGCAGCGAGGCGCGCGCTGGACGGTGTTCAGCGCGGGGAGG  
 ACGGGTCCGTGAACCTTCTCCGGGCTGGGACGCGTACCGAGACGGCTTGGCAGGCTCACC  
 GGGGAGACTGGCTCAAGGATCCAGCGCTGACCACAGGCTGCCTACGAGCTCACC  
 GCGGTGGACCTGGAGACTTTGAGAAATGGCAGCGCTATGCCGCTACGGGAGCTTCGGG  
 TGGGCTTGTTCCTGGACCTGAGGAAGACGGGTACCGCTCACCCTGGCTGACTATTCC  
 GGCACCTGCAGGCGACTCCTCCTGAAGCACAGCGCATGAGGTTCAACCAAGGACCGTGA  
 CAGCGACCAATTAGAGAACTGTGCCGCTTCTACCGCGGTGCTGGTGTACCGCAACT  
 GCCACAGCTCCAACCTCAATGGGAGTACCTGCGCGGTGCGCACGCTCCTATGCCGAGCGC  
 GTGGAGTGGTCTCCTGGACGGCTGGCAGTACTACTCAAGTTCTCTGAGATGAAGATCCG  
 GCGGTTCCGGGAGACCGCT**TAG**ACTGGTGCACCTTTCCTTGGCCCTGCTGGTCCCTGTGCG  
 CCCATCCCGACCCCACTC**ACT**CTTTCGTGAATGTTCTCCACCACTGTCCTGGCGGAC  
 CCACTCTCAGTAGGGAGGGGCCGGGCCATCCTGACACGAAGCTCCTTGGGCGGTGAAGT  
 CACACATCGCTTCTCGCCGTCCCAACCCCTCCATTGGCAGCTCACTGATCTCTTGGCTC  
 TGCTGATGGGGCTGGCAACTTGACGACCCCACTCCTGCTGCCCCACCTGTGACTCGG  
 TGCTGTTTCCGTCCTCGCAGGATGTGGAGTCTGCCCCAGGCACTCTGCGCTGCC  
 GGCCAAATACCGCATTTATGGGACAGAGAGCAGGGGACAGACACCCCTGAGTCCCTC  
 CTAGCAGATCCTGGCAATGTGAGTCTCTCTGAGGTGAGGTCTGAGGCGAGTATCCTCCAG  
 CCTCCCAATGCCAAGCCCAACCCGTTTCCCTGGTGCCACAGAACCCACCTCTCCCCAA  
 GGGCTCAGCTGCTGTGGGCTGGGTGGCCCATCCTACAGGCCCTGAGGTGAGGATGGG  
 GAGTCTGCTGCTTTGGGACCCACGCTCCAAGCTGAGACAGTTCCCTGGAGGGCCACCGAC  
 CTTGAGCCCGGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTGTG  
 TCTCAATGAGGCAACCACTCCCCACCACTGCCGGCCGCTCCTCACTGGGGAGC  
 CGGGCTGCCATCCCAATTCTCCTGCCTCGGAAGTGGGGTGGGGCTGACCCGTGGGGCT  
 GCACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGACGGCTGGGATGAG  
 GCTTGTACCAACCCCAACCAATTTCCAGGACTCCAGGCTCCTGAGGCCCTCCAGGAGG  
 GGCTTGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTCC  
 ATTGACCTGGCCACTGGACCCAGGCCAGGCCCGGCCCGCGAGTGGTCAAGGGACAGGGA  
 CCACCTCACCGGGCAAAATGGGGTGGGGGAGCTGGGGACCAAGCAGGACCACTGGACA  
 CTTTCTTGTGAATCCTCCCAACACCCAGCACCTGTCTATCCCACTCCTTGTGTGACACA  
 TGCAGAGGTGAGACCCGAGGCTCCAGGACAGCAGCAGCAGGCGAGGCTGGAGCGGG  
 CGCTTGTGCTCAGCTCCTCCTCGGAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA  
 GGTGCTCAGGGGTGTGGGGTTCCGTTCTCCCTCCCACTGAAGTTTGTGCTTAA  
 AACAAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCCGTGTGACTGGCTCTC  
 GTGCCAGTGCCACAGGTCATCCACATGCGCAG

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MVNDRWKTMGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAFLFNHHAHAPGT  
 APPPVVSTGAASANSALVTVTERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
 QPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHTLQGQLSALQSEQGRLLQLL  
 SESQGHMAHLVNSVSDILDALQDRDGLGRPNKADLQRAPARGTRPRGCATGSRPRDCLDVL  
 LSGQQDDGVYSVFPHTYPAGFQVYCDMRTDGGGWTFVQRRDGSVNFRRGWDAYRDGFGRLT  
 GEHWLGLKRIHALTTQAAELHVDLEDFENGATAYARYGSFGVGLFSVDPEEDGYPLTVADYS  
 GTAGDSLKLKHSGRMFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSLNGLQYLRGAHSAADG  
 VEWSSWTGWOSYSLKFSSEMKIRPVREDR

**FIGURE 229**

GCAGTCAGAGACTTCCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
 TGCTTCTCTGAAGTACAGTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTTCACTCT  
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
 ATGGGGACACCACATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC  
 TTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTCTGCAGCATGTGGC  
 TGAAAAACTCTGTCTGAGCTGTATAACAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAAATGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAGACAGCAAAAGTTGGGAG  
 GACTGTAATATTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA  
 CCTGGAAATTGCGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTTT  
 TCGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG  
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCTCAATGG  
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC  
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG  
 TTTCTGTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCAGTATTTAACAGTCACA  
 AGAAGTCTTATTACATGCCACCAACCTCAGAAACCCATAATGTCTATCTGCCTTCTTG  
 GCTTAGAGATAACTTTTAGCTCTCTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC  
 AGCAAATACACAAGGAATTCTTTTGTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG  
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCGGTTTCATATCAG  
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA  
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTCCATTGACCCATATTTATACCTTTACG  
 GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAAA

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**FIGURE 230**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVL  
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL  
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFA  
QSYSEFFYSYWTGLLRPDGSGAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAILNGMIFSK  
CKELKRCVCERRAGMVKPESLHVPPETLGED

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AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG  
CTGACTTTTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGNTGCAGCAT  
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACCACTTCCC

**FIGURE 232**

GCCGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC  
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGGGG  
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCCCCTCGGAGACTCCTTGTGCTGCT  
 CTGGGGGTTCCGGGGGGCCGGGACCCGCGTCCGGGCGCCATCGGGGCATCGCTGCTGCTG  
 TCGGTGCTGCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCT  
 GCTCAGCGCTCACTTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG  
 AGCTGCGCGCGCGCGGCAACCAACCGCGCGCGCGCGGCCCAACTCGGTGACGCCCCGAGCG  
 GAGCGCGAGAAGCCCGGGGCGGGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCTTGGCC  
 CTACCAACCTGACAGCCCGGCCAGGCGGCCAAAAAGGCGCTCAGGACCCGCTACATCAGCA  
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC  
 ACGCTGGGCTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC  
 GGCGCAGCGGGCCCGCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCAGGAGCGAC  
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCAGCGCGACGACTTTGAC  
 TGGTCTTCTCTGCTGCGCTGACACCACTACACCGAGCGCACGGCTGGCACGCCCTAACTGG  
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACCTGGGCGGGCCCGAGGACTTCATCGGCG  
 GAGAGCCCAACCCCGCGCTACTGCGCAGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG  
 TCGCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCGCGCCCTCA  
 CGAGTGGCTGGGTGCTGCACTTCTCGATGCCACCGGGTGGGCTGCACTGGTGACCAGAGG  
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGAGGCCAGTGACAGAGGGGACCTCAT  
 TTCCGAAGTGGCCCTTGACAGCCCAACCTTGTGCGTGAACCTGTGACATGTACCAGCTGCACAA  
 AGCTTTGCGCCGAGCTGAACCTGGAACGCAAGTACCAGGAGATCCAGGAGTTACAGTGGGAGA  
 TCCAGAATAACGAGCATCTGCGCCGTTGATGGGGACCGGCGAGCTGCTTGGCCCGTGGGTATT  
 CCAGCACCATCCCCCGGGCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA  
 GCACGCTTTTCTCTGCGCGCATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG  
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCAACCGGCGCTTG  
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGTACCAGCGCTTGTATCCGGCCCGGGGTATGGA  
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCGCAGGAGGCGCGCGGCCCTCACTC  
 GCGGAGTGCAGCTGCTCCGGCCGCTGAGCGCGTGGAGATCTTGGCTGTGCCCTATGTCACT  
 GAGGCCCTCAGCTCTCACTGTGCTGTGCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTGG  
 CTCTTGGAGGCGCTTGGCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC  
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGCACT  
 GTCAAGGCCACGCTGGCAGAGCTGGAGCGCGCTTCCCGGCTGCCCGGGTGCCATGGCTCAG  
 TGTGACAGACGCCCTCAGAACCAAGAGGAGCTGTGAGAGCGCTGGATCTCCAAGAGCACCCG  
 TGCACACACTGTTCTGCTGGCGGGCCAGACACGGTGCTCAGCGCTGACTTCTTGAACCCG  
 TGCCCGATGATGCCCAACCAAGGGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT  
 TTGATGCCAGGCGAGCCAGCGAGGCTGCTTCTACAACCTCAGCTACGTGGCCAGCCGCTGGG  
 CGCTTGGCGCAGCTCAGAACACAAGAGGAGCTGCTGAGAGCGCTGGATGTGTACGAGCT  
 GTTCTTCCACTTCTCCAGTGTGATGTGTGCGGGCGGTGGAGCGCGGCTGCTGACGCGCT  
 ACCGGCCCGAGAGCTGACGCGGAGGCTCAGTGAGGACCTGTACACCGCTGCCCTCAGAGC  
 GTGCTTGAAGGCGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTTTGAACAGGAGCAGGG  
 CAACAGCACTGACCCCAACCTGTCCCGTGGCGGCTGGCATGGCCACACCCCAACCCCACT  
 CTCCCCAAAACAGAGCCACCTGCCAGCCTGCTGGGCGAGGCTGGCCGTAGCCAGACCC  
 AAGCTGGCCCACTGGTCCCTCTCTGCTGCTGTGGGCTCCCTGGGCTGTCGACAGCACTGGG  
 GGAGCTGCCCCAGAGGCCACCACTTCTCATCCAAACCCAGTTTCCTGCCCCCTGACGCT  
 GCTGATTGCGGCTGTGGCCCTCCACGTATTTATGCAGTACAGTGTGCTGACGCGACCCCTGC  
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGAGGGG  
 GCATCTCCCACTTCTCCCTTTTGGACCCTGCCAAGCTCCCTGCCTTTAATAAACTGGCCA  
 AGTGTGAAAAA



**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQLLVAVL  
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE  
QHGDDEFDWFVLVPDDTTYEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAPVVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL  
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSDEL  
YHRCLQSVLEGLGSRTQLAMLLEFEQEQGNST

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**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCCTAGTGGAGAAAAGGAGT  
AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCCTTTGAAGATGAAAG  
ACTAGCGGAAGCTCTGCCTCTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
CTGTATCCACCCAAATGTCACCGATTTCCTTCTATGCAGGAAATGAGCAGACCCATCAATAA  
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG  
AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG  
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
TTCCCCGCCCCCTGAGACCTGCAGCACCATCTGTCATGGCGGCTGGGCTGTTTGGTTTGAGC  
GCTCGCCGCTTTTGGCGGCAGCGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA  
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC  
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA  
GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT  
CTTTGGCGTCTCCATCATCTCTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
GGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTG  
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCGCTGCCTGCCATTCTGAC  
CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE  
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

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T0611.1E/0850

**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAGCGGCCCCAGAACCGACCACCCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAACTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTCGACCCAGCA  
AGATCCAG

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**FIGURE 237**

GCGGCGGCT**ATG**CGGCTTGCTCTGCTCGTCTGCTGCTCGGCGCCGCGGCTGGTGCCT  
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCCGCTGCCTCCGGGG  
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG  
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA  
 GCTGCACCTGTCACTTACACAAAGGCTTTTGGAGGACCCGATACTGGGGCCACCCCTTCCTGC  
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA  
 TCTTGGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA  
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG  
 ACCACTACTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC  
 CCTTGGAAAGAGCTCTTGCCCTGTAGTTCGAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA  
 TCGCTTGTTCCACACAGCTACCACTCCAGGAGTGCATATCCGCCCTGTTTGCAGAAATG  
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCACTTGTATTGTATGCCTTC  
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCCGAACCCCTCACGGA  
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACAGGACA  
 ACGAGACATTAGAGGTGACCCACCCCGGACCTACATATCAGGACGTCATCCTTAGGCACT  
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTGAAACCT  
 CAACATCCAGCTCAAGTGGGAAGAGACCCCAAGAAATGAGGCCCCCCAGTGCCTTCCTGC  
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC  
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG  
 GCTGTATGTGCACACCTTCAACATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC  
 ACTACCAGCTGCCAGGACCGGCTGCAACCCCACTCCTGGAGATGCTGATTCACTGCGCG  
 GCCAAGCTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGCGCTGCTGAAGTGGACCGAGTA  
 CACGCCAGATCTTAACCATGGCTTCTATGTACAGCCATCTGTCTCCTCAGGCGCCTTGTGCCA  
 GCATGGTAGCAGCAAGCCAGTGGACTGGGAAAGAGATCCCTCTTCAACAGCCTGTTCCCA  
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACGTGGTGGCGGTGT  
 GCTACGGCTCCTTACAACTCTCCTCACCGAACCTTCCACATCGAGGAGCCCCGACAGGT  
 GGCTTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACT**CTGA**TT  
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT  
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACAGGTGAGGC  
 CTACAGCTGTGTTGCCGATACAGGAGCCACGACCCAAATGGGCATTTGAATTTGAATTA  
 CTTAGAAATTCATTCTTCCCTACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA  
 AGTGGTCGGTGGCTGCTGATTGGACAGCACAGAAAAAGATTTCCATCACCCACAGAAAGGTC  
 GGCTGGCAGCACTGGCCAAGGTGATGGGCTGTGCTACACAGTGTATGTCACTGTGTAGTGGA  
 TGGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSSISWELRQTLSSVVFDAFITG  
QGKKDWSLFRMFSTRLTPEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLLVLNLPDPFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

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**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCCAAGGACGGTACTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAAGTGCCTTTAAGAGACCCCAAAGAGCTGCCTTGGCCTTC  
TGCAATGTGTGATCAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAAGTGTGAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

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**FIGURE 240**

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

0000734.11901



**FIGURE 241**

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTGGCCAGG  
 AAACCTGAGCGGTGAGACTCCAGCTGCCATACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACCAGCCACCCACCACTAGAGGTCCTGCTGTGGAGATGCAGGCCACTTGAGCCAAAGG  
 CGTCCAGTGGTCTTGTTCTGGCTGTCTGGTCTTCTTCTCCTGCTTGCCTTGCCTCTTTTA  
 TTAAGGAGSCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT  
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCAAGGCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAAGACGACCCAAGGAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGAGC  
 GTGTCAAGAAAGCACCAGGGCAAAGCGGCAACCAAGCCAGGACGCTCATTTCCAAAAGTCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCTATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTCCAG  
 AGCCCCACGACGACAGAAACCAAAGACTGAAGGCCGCGCACTTCAAATCTAGCCTCGGTG  
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCTTCAGACGACTTGCCCTGACTCTG  
 TGAAGATCAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC  
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCAACACC  
 CTTTGGCTTCATGGAGCTCACTACTCTTGGTGCAAGGTCGTGACACGCTTCCTCCAG  
 TGCCCCAGCAGCAGTCTCTCTGGCCAGCCTCCCGCTGGGAGCCTCCGCTGCATCACTGT  
 GCCGTGGTGGGCAACGGGGGCATCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTATTAAAGGCTACGAACAGGATGTGGGGACTC  
 GGACATCTCTTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCGCTACTTGCATCTCTGGGAAGGCAC  
 CCGGGACTTGAAGGCTGGAAGCACTGCTTATGAATCAGACGCTGATGTCAAAAAACCTTT  
 TCTGGTTCAAGGCACAGACCCAGGAAGCTTTTGGGAAGCCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA  
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCTCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACGAGCCTCTGGTC  
 CCGGAACCTGCAAAGCCAAAGCACTGACCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGTCT  
 CAAGGCACAGGATACGTTGGGAATCTTGAGACTCTTGGCCATTTCCATGGCTCAGACTAA  
 GCTCCAAGCCCTTCAGGAGTTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAAATGGCTAATTGAGGTTCTGAAGTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG  
 GATTTTAAATTAATAGGCTGATGGGTGGCCAATACCAATCTCTGCTGAAAAACACTCTT  
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG  
 GTTTGAATCCAGATCAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACTTCACTAC  
 AGATTGCTAGAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGCTCATAGCTTGTCTGTG  
 TCTTTAAGCTATTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGT  
 TCCATGGAAGGCCAAATAAATTTTCTACAGTGAAAAA

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**FIGURE 242**

MRSLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTEINIKERSLQSLAKP  
KSQAPTRARRRTTIIYAEAPENNALNTQTQPKAHTTGDGRKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGAIVSTRTRQKGVTTAVIPPKEKKPQATPPPAFQSPTTQRN  
QRLKAANFKSEPRWDFEEKYSFEGIGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDLSRHF  
NQSEWDRLEHFAPPFGMELNYSLVQKVVTRFPVPQQQLLALSLPAGSLRCITCAVVGNGG  
ILNNSHMQGEIDSHDYVFRSLGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP  
LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREAHMDRYLLHLPDFL  
RYMKNRFLRSKTLGDAHWRIRYPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDYTSW  
KRLIFYINHDFKLEREVWKRHLDEGIIRLYQRPGPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTTCAGACAGACTCTTCCATAAGTCTTTGAGTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTATCTGTCACTTATTT

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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKH FHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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T06TT"42/08660

**FIGURE 245**

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCTGCGGTCCCTTCTCTGGGAGG  
CCCCAGCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCC  
CTCACCGCAATCGCTCTGTTGGTGTCTGGGGGCTCCCCGGTGTCTGGCCGGCAGGACTGCCT  
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTACCTTC  
GCTGCGGGACCTGCTACCATCGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG  
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
CCTCTTTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTGTGTCTCTGTGTGTACTCTGT  
ACCGCCGGCGCCAGCAGCTCCAGAGCCATTGTGAAGGCCAGGAGATTCCAATGACAGGCATC  
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
TGGCTTACGTACCCACCTAGTGGTCTGTCCCCAATATCCACTCTACCCAGCTGGGCCCC  
CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
**TGA**GGAAACAGCCATGTCTCTGTCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
CCTGTACCTGCATCTGGTCTCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCA  
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAAC TAGA  
ACTATGAGGGGTTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGC AAGGAGG  
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG  
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCCTCTGGGCTGGGGTGGGGGGAGGAGGAGGT  
TCCGTGACAGCTGGCAGTAGCCCTCTCTTGCTGCCCATGCCCACATCTCTGGCTG  
CTAGATTAAAGCTGTAAGACAAA

**FIGURE 246**

MPPAGLRRAPLTAIALLVLGAPLVLAGEDCLWYLDNRGSHWPGFNCEFFTCCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGFAPQYPLYPAGPPVYNPAAPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

**FIGURE 247**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCCAGAA  
 CCCAGGTAGGTAGAGCAAGAAGATGGTGTCTGCCCCCAAAATGGTCCCTTGCACCAATG  
 TCAATTTCTACTTTCTCACTGTGGCTCTCTTAACGTGTCCACTCCCTTCAATGGTTCAGAG  
 CACTGAGCATCTCCAAAACGTAGTGATGGGACACCATTTCTTGGAAATAAAATACGACTTC  
 CTGAGTAGCTCATCCCACTTATTATGATCTCTTGATCCATGCAAACTTACCACGCTGACC  
 TTCTGGGGAACCTGCAAAATAGAAAATCAGCCAGTCAGCCCCACAGCACCATCTCTGCA  
 TAGTCAACCCCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG  
 AAGAACCCTGCAAGTCTCTGGAACACCCCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG  
 CCCCTCTTGTGCGGCTCCCGTACACAGTTGTCAATCACTATGCTGGCAATCTTTCGGAGAC  
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGAAGTATACAGAT  
 CAACCAAAATTTGAACCACTGCAGCTAGAATGGCCCTTCCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC  
 ATTGGTGAATCTGTGACTGTTGGCTGAAGGACTCATAGAAGACCAATTTTGATGTCACTGTGA  
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTAGATTTTGAAGTCTGTGACGAAGATAACC  
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCACAGACAAGATAAAATCAAGCAGATTATGC  
 ATCTGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTTATTCAGCATACCGTATCCCC  
 TACCCAAACAAGATCTTGTGCTATTCCGACTTTTCAGTCTGGTGTATGGAATACTGGGGA  
 CTGACAAATATAGAGATCTGCTCTGTTGTTGATGACAGAAAAGTCTTCTGCACTCAAGTAA  
 GCTTGGCATCAGATGACTGTGGCCCATGAACCTGGCCCAACAGTGGTTTGGGAACCTGGTCA  
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG  
 TCTGTGAGTGTGACCACTGAACTGAAAGTTGGAGATTTTCTTTGGCAAAATGTTTGTGA  
 CGCAATGGGAGTATGCTTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAATAATCCTG  
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGAGTGGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTATAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG  
 ATGGTATAAAGGGATGGATGGCTTTTGTCTAGAAATCAACATTCATCTTCTCCTCACAT  
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACATGCGAGAGGGGTTT  
 TCCCTTAATACCATCAGATGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA  
 AGGCTCTGACGGGCGGCCGGACACTGGGTACCTGTGGCATGTTCACTTACATTCATCACC  
 AGCAAAATCCAAATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC  
 AGAAGAGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTGCATTAG  
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACAGCAGTCAAGCAGT  
 AATGATCGGGCAAGTCTCATTAACAATGCATTTGACCTCGTCAGCATTTGGGAAGCTGTCCAT  
 TGAAAGGGCTTTGGATTTATCCCTGTACTTGAACATGAAACTGAAATTTATGCCCGTGTGTTT  
 AAGGTTTGAATGAGCTGATTTCTATGATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG  
 GAAACTCAATTTCAAGGCTCTCTCTCATCAGGCTGCTAAGGGACCTCATGTAAGCAGACATG  
 CACAGACAGGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG  
 TGCAACAACTACAGCCGTGCGTACAGAGGCGAGAAGGCTATTTGAGAAAGTGGGAAGGAATG  
 AATGGAACCTTTGAGCCTGCCCTGCGAGCTGACCTTTGGCAGTGTGCTGTGGGGGGCCACAG  
 CACAGAGGCTGGGATTTCTTTATAGTAATATCAGTTTCTTTGTCCAGTACTGAGAAAAA  
 GCCAAATTTGAATTTGCCCTGCGAGAACCCAAATAAGGAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTACACTCATTGG  
 CAGGAACCCCACTAGGATACCCACTGGCCCTGGCAATTTCTGAGGAATAAACTGGAAACAACTTG  
 TACAAAAGTTTGAATCTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAAACAAATCAA  
 TTCTCCACAAGAACCGGCTTGAAGAGTTAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG  
 TTCTCAGCTCCGTGTGTCCACAGACAATTGAACCAATGAAGAAAAATCCGGTGGATGG  
 ATAGAATTTTGAATAAACTCAGAGTGTGGCTGCAAGTGAAGAGTTGACGTATGTGAAAAA  
 TTCTCCCTTCCCGGCTTCTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTGTTGGCTCCAACCTGGAGATCTTTTCCCTCAACTCATCTTTTGA  
 CTATCCCTGTGAAAAGAATAGCTGTTAGTGTTCATGAATGGCTTTTTCATGAATGGGTTA  
 TCCTACCATGTGTTTGTGTTTCTCATCAGGTTGTGCCCTGCAACGTAAACCAAGTGTGGGT  
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
 YDLLIHANLTTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE  
 HPPQEQIALLAPEPLLVLPTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
 ARMAFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA  
 I PDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWWNDL  
 WLNIEGFAKFMEFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTFVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDSG  
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
 MYKLEKMRDMNEVETQFKAFLIRLLRDLIDKQWTDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTESKSQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEFPPQILTLIGRNPVGYPLAWQFLRKNWNKLQVKFELGS  
 SSIAHVMVGTTNQFSTRRLLEEYKGFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360



**FIGURE 249**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGCCCTCCTGGGGTTTCATCCTCCCAC  
 TGCCAGGAGTGCAGGCGCTGCTGCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGCAATTGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGTGACGCG  
 AGGCCAAGGACCAGGAGCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCTGATC  
 TCCTACACCTTCGTGTGCCCGCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT  
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTCTGACCTGTATCGGGGGACCACCATATGACACACGGAAC  
 TTGGCTCAAGAACCACCTGATGGACCACATCGAATACCGAGATGTGCAGGTTGGGCGAGGT  
 GTGTCAGGAGACGCTGTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT  
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
 GCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGTGTCCACCAAAAT  
 GAGCATTACAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTT  
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATATCTACTCACCTAACAGCA  
 ACACTGGGGAGAGCCTGGAGCATCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

**FIGURE 250**

MSAVLLALLLGFILPLPGVQALLCQFGTVQHVWVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCFPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSTNTEMCEVGVCQETL  
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC  
PSC

CGCAGCGGGCAGGACGCCCGCTTCGCCTAGCGCGTGTCTCAGGAGTTGGTGTCTCGCTGCGCT  
CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCA**A**AGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCTG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGTCAT  
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCTAATGGAGAACAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGTGTGCGC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGTCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCACAGTGTCTGCCAGGGCCGCGGGGACAGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCTGGCCCGTGTCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACA  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
GAGAACATG**TGA**CGCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCTCTCGAGGGT  
GGCAGGGACAGACCCAGACCATGGTGGCAGCCAGGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGCTGTTGTCTTA**ACT**AGAAAAATGGCCATGCTTAAAGAGAAAAATG  
AAAGTCTTCTCGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

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**FIGURE 252**

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG  
PTGEKGDMDKGQKGSVGRHGKIGFIGSKGEKGDIGPPGPNGEPGLPCECSQLRKAIGE  
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCEFDKENM

09080734.11901

**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCTTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCAGAAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTACCTTTCTCTTCCCTGTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTCTACCTGACCTGGTGTGGAAACTGCA  
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAATAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 254**

MRIMLLFTAILAFSLAQSGFVAVCKPEQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKEKTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRP

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

GGGCGTCTCCGGCTGCTCTATTAGACTGTCTGCTGCTGTGCCCGCTGTGCCCTGCTGTGCC  
CGCGCTGTGCGCGCTGCTACCGCTGTCTGTGGACGCGGGAGACGCCAGCAGCTGGTGATTG  
GAGCCCTGCGGAGAGCTCAAGCGCCAGCTGTGCCCAGGAGCCAGGCTGCCCCGTGAGTC  
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCGGTGGTGTCATCCCCCTTGGGGC  
TGCTGTTCTTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCAC'TCTCTTAGAGGAG  
CTGCTCAGCAAATACCAGCACAAAGAGTCTCAC'TCCGGGTCGCGAGAGCCATCCCCAGGGA  
GGACAAGGAGGAGATCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC  
CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG  
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT  
TTGAGACAGGGTCTCAC'TCTGCCACTGACGCTGGAGTGCAATGGCAACAATCGCTACGCCCTG  
AAACCTTAGACTCCCGGGGTAAACGATCCTGCTTAGCCCTCCCAAGTAGCTGGAAC'TACAG  
GCATGCACCATAGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT  
TGCCAGGCTGGTCTTGAACTCTTAGGCTCAAGCAATCTCTGCTCAGCCTCTCAAAGTG  
CTAGATTATAGGATAGTGCACCCGTGTCTGGCTCTGGCTCTGTTCTTAACATTTGCCAAA  
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC  
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG  
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACAGCTAGCTGCACCACCTGACTTCTC  
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCTCGGCTGGTGGCATGACT  
GTGAGATAAGTCAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG  
CTTTGCTAACC GGGAAGAGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGGT  
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG  
TGAAACTTCCTTCTTGCTGTTTTTCCAGAACTACAGAGGAATGGACCACAGTCTCCAGG  
GTCCC'TCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTACGCTATGAATGGCT  
TTTAAACAAACCCACGTCCCAGCTGGGTAACTGGTAAGGCCCGCTCTACAAAAAAATC  
CAAGTTAGCCGGGACGTGTGGTGCACCTGTAGTCCGAGCTGACGTGGGACTGAGGTGGAG  
TGAGGTAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC  
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCAAAA

**FIGURE 256**

MSCVLGGVIPLGLFLVCGSQGYLLPNVTILLELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGR  
GGSLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**TAT**GGG  
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG  
TGTCCCTTCTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT  
CAGCAGGCCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 258**

MGSGPLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS  
VTLHHARSQHVVVCNT

1991

**FIGURE 259**

AATTGTATCTGTGAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAACGTTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG  
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCTCC  
CTCCGATTGTTCTAAAT**TAA**TTGAAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCIC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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**FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

00000731.11301

**FIGURE 261**

GAGGATTTCGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT  
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTT  
 CGAGGAGCTTCTGCATTGCTGGTCTGTTCCTTGCAGCTTTTCTGCCCCGCCGAGTGTAC  
 CCAGGACCCAGCCATTGGTCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG  
 AAAAAATGTACCAAGCAACGAGGGGCATACATTCAAGAATTCGAAGAGTCTCAAAAAATATA  
 TCTGTCTATGCTGGGAAGATTGTACAGCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT  
 GGCACGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAACTCTCGAGAGGCTG  
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTGTGCCAAGAGCTGAAGAA  
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC  
 TTTGAAAAATAGTGAAGAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
 ACTCTCCAAAGGTGACTTTATTAATTTGGATCCAGAACAACACTGTTTGGGAATTTGCAAAC  
 ATACGGGCATTCTGAGGAGTAAACCAAGCCAGCTCCCCGGAAGCAATCCTAACACTTTC  
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGTTTTCTATTTTTTCAACCAAGCAACTT  
 CTAATGAGATAATCAAATATAACCTGCAGAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
 GGAGGGGTAGGCCGAGCATTGGTTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT  
 GGATGACATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCCATAGGCCATTTGGTCTCA  
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCATGCAGAAGCCAG  
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA  
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC  
 CCAACTGTCTTCTCCCAAGAGACCAAGAAGTCACTCCATTGATCCATTACAACCCAGAGAT  
 AAGCAGCTCTATGCTTGAATGAAGGAAACCAGATCATTACAACTCCAGACAAGAGAAA  
 GCTGCTCTGAAGTAATGCATTACAGCTGTGAGAAAGAGCATTGTGGCTTTGGCAGCTGTTT  
 TACAGGACAGTGAAGCTATAGCCCCTTCACAATATAGTATCCCTTAATCACACACAGGAAG  
 AGTGTGTAGAAGTGGAAATACGTATGCCTCTTTCCCAATGTCACTGCCTTAGGTATCTTC  
 CAAGAGCTTAGATGAGACATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA  
 CCTCCTGGCTCTCAAGGATGACCACATCTGATACAGCCTACTTCAAGCCTTTTGTGTTTACT  
 GCTCCCCAGCATTACTGTAACTCTGCCCCTCTCCCTCCCAATTAGAGTTGTATGCCAGC  
 CCTAATATTCCACACTGGCTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTT  
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCACTAAAATACTATTAATATTTCTTT  
 CTTTTCTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACTCC  
 AGAGCTCAAGAGATCCTCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
 CACACCTGGCTTAAATACTATTCTTATTGAGGTTTAACTCTATTTCCTTAGCCCTGTCT  
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATATAACATTTGAATATCGCTTT  
 CCAGGTGTGGAGTGTTCGCACATCATGAAATCTCGTTTCACTTTTGTGAACATGCACAAG  
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTAACAAGTGAAGATACAGC  
 TAGAAAAATCTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAATACGTATGTT  
 GTTTACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC  
 TTTAGCGAGTTTTCATGTCTGCACAAGACCTTTCAATAGGCCCTTTCAATAGATTAATCCCTCC  
 AGAAAACCAAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTTGTCTTGTCTGCTCTGT  
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

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 106111.12266660

**FIGURE 262**

MMVALRGASALLVFLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL  
QEAEKKIRTLNASCNMLMGIKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

09989734.111901

**FIGURE 263**

GGGCGCCCGCTACTACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA  
 TGTGCGGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG  
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGGCCGGCCCGCTGCCAAAAAGC  
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC  
 GGAAGGAGAAGCCTCAACAAACAACCTTCACCCACCGCCTCTGGCTCGAGCTCTGAAGAGC  
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC  
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA  
 TGAGAGCCAACTGGAGCTGGACCACGCCACCTGGTGGCGTTCAGCCCTGACTGCAGAGCC  
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTGCTTCAAGATGACCAAGCGGGAGGA  
 TGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAGGCGCTGTCA  
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC  
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAACAC  
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA  
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGGAGTTCAGGAGGTGGTGCAGCCTTCGAA  
 CTAAAGGGCCACTCCGCGCTGTGCACTCGTTTGCTTCTCCAACGACTCACGGAGGATGGC  
 TTCTGTCTCCAAGGATGGTACATGGAACATGTGGGACACAGATGTGGAATACAAGAAGAAGC  
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGGGCGGGGTGCCGCGCGTGGCCG  
 CTGGCCCTCTCCCCAACGCCACGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTATCTCTA  
 CAATACCCGGCGGGCGAGAAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA  
 ACTTGTCCCTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGGCTG  
 TTTCACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC  
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTTGA  
 AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGCGCGCAGAGGATTGAGGAGGAG  
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCCTCCAGGTGGAAGCCTTTGAGAAGG  
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCCATGAACTACTCTTGTCTACTT  
 AGGTCTCTCTTCTTCTGCTGGCTGTGACTCCTCCTGACTAGTGGCCAAGGTGCTTTTCTTCT  
 CTCCAGGCCCATGGGTGGAATCTGTCCCACTGGCACTGAGGAGAATGGTAGAGAGGAG  
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAG  
 TTTGTAATGTTCCAGAACAACCTAGAGAACCTGAGTACTAAGCAGAGTTTTGCAAGGA  
 TGGGAGACTGGGATAGCTTCCCATCACAGAACTGTGTCCATCAAAAAGACCTAAGGGATT  
 TCCTTCTGGGCCCTAGTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTGCA  
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAAGTAGAAAAAGT  
 AGTACTATTGCTCAATGCTGAAAGTGTAAGAGTGGGAACCACTGTGCTTTGAAACCAAT  
 TTAGAAACACATTCCTTGGGAAGGCAAGTTTCTGGGACTTGATCATACATTTATATGCT  
 TGGGACTTCTCTCTTCGGGAGATGATATCTGTTTAAAGGAGACCTCTTTTCAGTTTCATCAAG  
 TTGCATAGATATTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAAAAAA  
 AA

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**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQRIKKEKPQQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFSPCRAFIWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSLKGQVLSTINTNQMNNTAAVSPCGRFVASC  
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

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**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
 CAGTGTTTTGCCTTACCCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC  
 TCCTAGTAAGTGTGTCTGACTGTGCTGTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGT  
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGT  
 GGGCGGGAAGGCAGGAGTGCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA  
 AGCACACACCTGTCTTGTCTGCCAACCTGTGTGCTCCAGGTTCCCGGACGGCAGGTAC  
 CGCTGTCTCCATGGACTTGAAGAACATCAATTTT**TAG**CGCTTGCTGGTCTCAGGATACCA  
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC  
 TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG  
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG  
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
 AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCAGGTGACCTGCTCTCTTTCTGGGCCCTG  
 CCCCTCTCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT  
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG  
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC  
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
 CCTGTGACCTTCTGCCAGAATTGTATGCCTCTGAGGCCCTCTTACCACACTTTACCACT  
 TAACCACTGAAGCCCCCAATTCCACAGCTTTCCATTAAATGCAAATGGTGGTGGTTCAA  
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCA  
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG  
 TGGGAGCAAGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTTCAGACCAGGGAGG  
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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**FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCH  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAGGCCGCGCAGAAGGGAGGCACCTTGAGAAATGTCTTTC  
 CTCCAGGACCCAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
 CCTTGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA  
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG  
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT  
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG  
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTTGGTGATCA  
 GGAAAGCAGGCATTCTTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACT  
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT  
 TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT  
 GTTTCCTACTCGTGTCCCTAAGGAGTGAGAAACCAATTATACTCTACTCTCAGTATGGATTA  
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGC AAAATAGCCCCAAAACAAGACTGA  
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA  
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG  
 TGAGCAAGTCACCTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG  
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
 CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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**FIGURE 268**

MSFLQDPSFFTGMWWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCGAGGAACCTGAGCTAGGTCAAAGACGCCCCG  
GGCCAGGTGCCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCCATGGCGGAACCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGCCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG  
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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**FIGURE 271**

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT  
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTTCTGTCACTATTATTATTGTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTAAAGGCAAATACACATATTAGTATTACCTTAGTGTAAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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**FIGURE 273**

GCCAGGAATAACTAGAGAGGAAC**AATG**GGGTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT  
 GTGCCCTGCTGCACCAGTCAAACTACTCTCTTATTAGCTGAATAATAAGGCTTTGAAGATA  
 TTGTCATTTGTTATAGATCCTTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT  
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 TGTATCTATATTAATCTCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAAGCCAAACATG  
 AAAACCATAAAGATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCA  
 TACACCAACAGCTTACAGAAATGTGGAGAGAAAGCCGAATACATTCACTTCACCCTGACCT  
 TCTACTTGGAAAAAAACAAATGAATATGGACCACCAGGCAAACCTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGAGCTGTTTATGAGTACAATGAAGATCAGCCTTTCTACCGTGTAAAG  
 TCAAAAAAAATCGAAGCAACAGGTGTTCCCGAGGTATCTCTGGTAGAAAAAGAGTTTATAA  
 GTGTCAAGGAGGAGCTGTCTTTAGTAGAGCATGCAGAATTGATTTCAACAAAAAAGCTGTATG  
 GAAAAGATTGTCAATTCTTTCTGTATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG  
 CAAAGATTATGATCTGTTGTTGAAATTTGTAAACAAAAACCCATAATCAAGAAGCTCCAAG  
 CCTACAAAAACATAAAGTCAATTTTGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATT  
 TTAACAAACCATACCATGTGTGACACCACTCTCCACCTGTCTTCTCATTTGCTGAAGATC  
 AGTCAAAAGATTGTGTCTTAGTCTTGTATAAGTCTGGAAGCATGGGGGGTAAAGACCGCT  
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAATGGATCCTGGG  
 TGGGATGGTTCCTTTGATAGTACTGCCACTATTGTAATAAGCTATTCCAAATAAAAAGC  
 AGTGATGAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAATCTCAT  
 CTGCTCTGAAATTAATATGCATTTCAAGTGATTGGAGAGGTACATTTCCCACTCGATGGAT  
 CGGAAGTACTCTCTGACTGATGGGAGGATAACACTGCAAGTCTTGTGATTGTGAAGTG  
 AAACAAGATGGGGCCATTTGTTCAATTTATGCTTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
 AGAGATGAGCAAGATAACAGGAGGAAGTCAATTTATGTTTCAGATGAAGCTCAGAACATG  
 GCTCATGATGCTTTTGGGCTCTTACATCAGGAATACTGATCTCTCCAGAGATCCCTT  
 CAGCTCGAAATGAAGGATTAACACTGAATAGTAATGCCCTGGATGAACGACACTGTCAAT  
 TGATAGTACAGTGGGAAAGGACAGCTTCTTCTCATCACATGGAACAGCTGTGCTCCCGATTA  
 TTTCTCTCTGGGATCCCACTGGAAACAAATAATGGAAAAATTCACAGTGGATGCAACTTCCAAA  
 ATGGCCTATCTCAGTAAATCCAGGAACATGCAAGGTGGGCACTTGGGCATCAATCTTCAAGC  
 CAAAGCAACCCCAAGAACTTAACATTTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGC  
 CTCCAATCAAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATT  
 GTTTTACGCAAGAAATCTACAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCAAT  
 TGAATCACAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT  
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAAATGGCAGATAT  
 AGCTTAAAAAGTTCCGGCTCATGGAGGAGCAAACTGCCAGGCTAAAAATTACGGCTCCCAT  
 GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTTGAAGCAAAACCGCCAA  
 GACCTGAAATTTGATGAGGATACCTCAGACCACCTTGGAGGATTTCAGCCGAACAGCATCCCGGA  
 GGTGCAATTTGGTATTCACAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATCTTACATGGACAGCACCAG  
 GAGATAATTTTGAATGGGAAAGTTCAACGTTTATATCATAGAATAAGTGCAAGTATCTT  
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA  
 GGCCAACTCCAAGAAAGCTTTGCATTTAAACCAAGAAATATCTCAGAAGAAATGCAACCC  
 ACATATTTATTTGCCATTAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT  
 GCACAAGTAACCTTTGTTTCCCTCAAGCAAACTCTGATGACATTGATCCTACACTCATCTC  
 TACTCTCTACTCTCTCTGATAAAAGTCATAATTTCTGGAGTTAATTTTCTACGCTGGTAT  
 TGTCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTAAAGTACCACCATTTGAACCTTA  
 ACCAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTAAAAACAAAAAATGTAAGT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAATAATT  
 TTAAGATGTCGGAAGAGGATCTTTGATTTAAATAAAACACACTCGGATATGTAATAACTGT  
 CAAGATTAATAATTAATGTTTCAATTTATTTTATTTTATTTGTAAGAAATAGTGATGAAC  
 AAAGATCTCTTTTCACTACTGATACCTGGTGTATATTTTGAATGCAACAGTTTCTGAAAT  
 GATATTTCAAATTTGATCAAGAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAA  
 GGAGAGCAAAATAACAACATTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MGLFRGFVFLVLVCLLLQNSSTFIKLNNGFEDIVIVIDPSVPEDEKIEIQIEDMVTTASTY  
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC  
GEKGEYIHTFPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFPDVKQTEKASIMFMQSIDSVVE  
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVPVFSLLKISQRIVCLV  
LDKSGSMGGKDRLNRMNQAAKHFLLTQTVENGSSWGMVHFDSTATIVNKLIQIKSSDERNTLM  
AGLPYTPYLGSTSCSGIKYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKKQSGAIVH  
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGTDLSQLQLESKGLT  
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG  
TAKVGTWAYNLQAKANPETLTIITVTSRAANSVPPITVNAKMKNKDVSFSPSMIVYAEILQG  
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQDGVYSRYFTTEYDENGRYSLKVRAG  
GANTARLKLRPPLNRAAYIPGWVWNGEIANPPEIDEDQTYTLEDPSRTAGGAFVVSQV  
PSLPFLPDQYPPSQITDLATVHDEKILITLTPAGDNLDVGVKQVRYIIRISASILDRDSFDD  
ALQVNTDTPDPSPEANSKESFAFKPENISEENATHIFIATKSIDKSNLTSKVSNIAQVTLFIP  
QANPDDIDPPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

## amino acids 1-21

## amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 275**

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAGACCGGGAAAGACCATACGTCCTCCG  
 GGCAGGGGTGACAAACAGGTGTCTCTTTTGTATCTCGTGTGTGGCTGCCTTCTCTATTCAAGGAAG  
 ACGCCAAAGTAAATTTTGACCAGGAGCAATGATGTAGCCACCTCTCAACCTTCCTCTCTTGAAACC  
 CCCAGCTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTTT  
 GTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTTGTAGCAGTCTCAGAAGTGAATGCTTGCCTGA  
 GGGTGGACAGAGAAAGGAAGGTCCCCCTTTGCTGTTGTGGCTGCACATCAGGAAGGCTGTGATGGG  
 AATGAAGGTGAAACTTTGGAGATTTCACTTCAGTCTGTTGCTTCTGCTGCAAGATGATCTGTTTAAAA  
 GTAGAGAAGTGTCTGTGTGTGTGTTAACTCCAAGAGGCGAGAAGTCTGTCTAGAAGGAATGGATGT  
 CAAGCAGCTCCGGGGGGCCAAACGCATGCTTCTGTGCTAGCCGAGGAAGCTCCTCCGTGGGG  
 GCGCCGGCTTTGAGGGATGCCACCGGTCTGTGGACGATGGCTGATTCCTGAATGATGATGGTTCGCC  
 GGGGGCTGCTTTCGCTGGATTTCCCGGGTGGTGGTTTGTGGTGGCTCCTCTGCTGTGCTATCTCTCT  
 CCTGTACATGTTGGGCTGCACCCCAAAGGTGTGACGAGGAGCAGCTGCATCTGCCAGGGCCACACG  
 CCCACGGGGAAGGAGGTGTACAGGCTCTCTCAGAGTGGGAGGACGACCCCACTACGTGA  
 CGAGCTGAACGGCAGATCGCACGCTCAAGGAGGAGCTCAGGAGAGAGTGTAGCAGTCTCAGGAA  
 TGCGCAGTACCAAGCCAGCAGTGTCTGTGGCCTGGGCTGTGACAGGAGCCCCCAGAGAAAAACCCAG  
 GCCAGCTTCTGGGCTTCTCACTCGCAGGTGGACAAGGCAAGGTGAATGCTGGCTCAAGCTGG  
 CCACAGAGTATGCGAGCAGTGCCCTTCGATAGCTTTACTCTACAGAAGGTGTACACGCTGGAGACTGG  
 CCTTACCCGACACCCGAGGAGAAGCCTGTGAGGAGGACAAGCGGATGAGTTGGTGGAGCCATT  
 GAATCAGCCTTTGGAGACCTTGAACAATCCTGCAGAGAACAGCCCCAATCACCGCTCTTACCGGCT  
 CTGATTTTCATGAAGGGATCTACCGAACAGAAAGGACAAGGAGCAATGTTATGAGCTACCTTTCAA  
 AGGGGACCAACAAACGAAATTCACACGGCTCATCTTATTTCCAGCAATTCAGCCCATATGAAAGT  
 AAAAATGAAAGCTCAACATGGCCACACGCTTATCAATGTATCTGCTGCTCAGCAAAAGAGGGTGG  
 ACAAGTTCCCGGCACTCATGCAAGATTTTCAGGAGAGTGTGCATTTGAGCAGGATGGGAGAGTCCATCT  
 GCACTGTTGTTTACTTTGGGAGAGAAATTAATGAAGTCAAGGAAATCTTCAAAACCTCCAA  
 GCTGCGCACTTCAGGAATCTTACCTTCAATCAGCTGAATGAGAGATTTCTGCGGGAAGGAGCTTG  
 ATGTTGGAGCCGCTTTCAGGAGGAACCAACGCTCTCTCTTTTCTGTGATGTGGAATCTTACTTT  
 CACATCAATTTCTCAATAGCTGTAGGCTGAATACACAGCCAGGGAAGAGATTTTATCAGATT  
 CTTTTCAGTCAGTACAATCCTGGCATATATACGGCCACCATGATGCAAGTCCCTCCCTTGGACACG  
 AGCTCGCTATAAAGGAAGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCAATATCG  
 GTACAGCTTTCATCAATATAGGTGGGTTTGTCTGGACATCAAGGCTGGGGCGGAGGAGTGTGCAC  
 CTTTATCGCAAGTATCTCCACAGCAACCTCATATGGTACGGAGCTCTGCGAGGACTTTGCCAC  
 TCTGGCATGAGAGCGGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAAGTCCAA  
 GGCCATGAACAGGACCTCCACGGCCAGCTGGGCATGCTGTGTTCAGGACAGAGATAGAGGCTCAC  
 CTTCCGAAACAGAAACAGAACAGTAGCAAAAAACATGCACTCCACAGAGAAGGATTTGGGGAGA  
 CACTTTTTCTTTCTTTTGGCAATTTACTGAAAGTGGCTGCACACAGAGAAAGACTTCCATAAAGGAC  
 ACAAAAGAAATTTGGAATGTGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTAC  
 AACAGAAATCAAAATCTCCGCTTTGCCGTCAAAAGTAAACCAAGTTGCACTCTGTGAGTCTGTGCA  
 AAGGCAGAAATGCTTGTGAGATTTAAGCCTAATGTTGGAGGTTTGTGCTGTTTCAATACACT  
 GAGCCTGTGTTTGTGTCTTATGAAATATTCATGATTTAAGACAGTTTTGTAAAAAATTCAT  
 TAGCATGAAAGGAGGACATATTTCTCCATATGAATGAGCCTATCAGCAGGCTCTAGTTTCTTAGG  
 AATGTCTAAAAATCTCAGAAGGCGAGGAGGAGATAGGCTTATTATGATCACTAGTGAGTACATTAACTA  
 AATAAAATGGACCAGGAAAGAAAGAAACATAAATCTGTGTCAATTTTCCCAAGATTAAACA  
 AAAAATAATCTGCTTATCTTTTGTGTTGCTTTTAACTGTCTCCGTTTCTTTTCTTTTATTTAAAAAT  
 GCACTTTTTTTTCTTCTGTGAGTTATAGTCTGCTTATTTAATACCACTTTGCAAGCCTTACAAGAGA  
 GCACAAAGTTGGCCTCAATTTTTATTTTTAAGAAGATACCTTTGAGATGCAATATGAGAACTTTCA  
 GTTCAAGACTACATTTGATGCCATATCCAGGACATGCCAAATGCTGTTCTGTCAAGCTGAAT  
 GTCCAGGCTTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGCGTACAGATCTTTCTCTGAA  
 GAGTATTTTCGAAGAGGAGCACTGAACACTGGAGGAAAGAAATGACATTTCTGCTTACAGAA  
 AAGGAACTCATTCAGCTGTGTATCTGTGATGTACTTAAAGTCAAGACACACTTTCTCTCTCA  
 GAGTAGGAGACGCTTTCTTACCTTTTAAATACAGTATACCTGTGAACCAACAACTCTCT  
 TTTCAAAAAGGCTGCTCTCTCTGCTTCTGCTTCCATAGAAGAATGAGAAAAATATATATAT  
 ATATATATATATTTGAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTGTGCTACAT  
 GTTATCAACCCAGGCGAGGTGGAAGTAACTGAATTTTAAATTAAGCAGTCTTCAATCAATCA  
 CCAAGATGCTTCTGAAATTTGCAATTTTATTACCAATTTCAAACATTTTAAAAAATAAATACAGTTA  
 ACATAGAGTGGTTTCTTCACTCATGTGAAATTTATTAGCCAGCACCAGTGTGCATGAGCTAAATATCT  
 CTTTGAAGTCTTGTCTTGTGTTGCTCAGTAACTCATTTGTTTAAAGCTCAAGAACCTCAAGC  
 TGTGTGTGTGTTAAAAAATGCATTTGATTTGATGCTGGTATTTTGAATTTTAAATTAATAAACAC  
 AGGCCATGAATGGAAGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

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**FIGURE 276**

MMVMVRGGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFI  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES  
ALETLNPPAENSNNRPHYTASDFIEGIYRTERDKGTLTYELTFKGDKHKEFKRLILFRPFSP  
MKVKNEKLNMANLINVIVPLAKRVDKFRQMNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR  
LNTQPGKKVFYPVLFSSQYNGPIIYGHHDVPPLEQQOLVIKKEGTGFWRDFGFGMTQCYRSDFI  
NIGGFDLDIKGWGGEDVHLYRKYLHNSLIVVRTPVRGLFHLWHEKRCMDDELTPQYKMCMS  
KAMNEASHGOLGMLVFRHEIEAHLRKQKQKTSKKT

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GAAAAGA**ATGT**TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACCTGTGCAAC  
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
ATGCGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAA  
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT  
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTCTGCTGTTGAGGTGC  
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT  
CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTACTGATTTTAT  
CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
AAGTGTGAAAACATGATCACAAATGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG  
GGGCATATTAATGATGCCTTCA**TGA**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
TGTTCTGCTTCTCAAGAAATAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
CCAAGAGCAGATCATATATTTTGTGTTTCAACATTCTTCTTTTGAATAAAATTTTGAATGTGCT  
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC  
TCAAAATATTCTAAAAATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG  
TAGTTATTGATTTAAGCATTTTTAGAAAATAGATCAGGCATATGTATATATTTTACACACTT  
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATGTGTTGAGAAATCAT  
TGAAAATGGATCCTTTTTGACAGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAG  
TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAAT  
TTATCTCTTTATACACCAACAGTTGATTATATATTTCTGAATATCAGCCCTTAATAGGAC  
AATTCATATTGTTGTGACCAATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
TAATATATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 278**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQ TLE  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMPS

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AACCTCAAACCTCCTCTCTCTGGGAAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG  
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**  
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAAGAGCTCACAGCTCTTTGG  
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATG  
TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA  
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
CAACCCATGAGTGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTAGCA  
TGCCTCCATCCTTCTCTGGAAACTGCAGTTGACGACAATGGGACATACACTGCCAGGTGA  
AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCTGTGCACACTGTA  
CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
AATAGTAATTGTAGTGGTCTCTTCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
GTTTATTTAGAAGACACAGACT**TAACA**ATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA  
GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
TTTCCAACAGTCTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
AGTGTCTCCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAA  
GTGTAATATTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCTTAA  
GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAAGCC  
AATTTGTCTGTATACATTTCCCTTTCACGATTTCTTTTAGCAGCACTTCTGCTACTAAAGTCA  
ATGTTGTTTACTCTTTTCCCTTCCACATTTCTCAATTAAGGTGAGCTAAGCCCTCTCGGTG  
TTTCTGATTAACAGTAAATCTAAATTCAAACTGTTAAATGACATTTTATTTTATGTCTC  
TCCTTAACATATGAGACACATCTGTTTTACTGAATTTCTTCAATATTCCAGGTGATAGATT  
TTTGTGCG

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**FIGURE 280**

MYGKSSTRAVLLLLLGIQLTALWPFAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVGVIQEIRLSVVHTVRFSEIHFLALAIGSACALMIIVIVVVLQHYRKKRWAER  
AHKVVEIKSKEERLNQEKKVSVYLEDTD

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**FIGURE 281**

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCGATGCTGAAACCACTGCTGCT  
GCAACCACCTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCTGTGATTTC  
ATCCAACTACTTACCTTGCCTACGATATCCCTTTATCTCTAATCAGTTTATTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT  
TAASTTARKDIPVLPKWVGDLNGRVCP

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**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTTGCCGAGAGA  
GTGTCTGGGTGAGGACGACAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCACAGGCTGG  
ATTTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATAAAAGTGAAGAA  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAAATGTTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCACTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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**FIGURE 285**

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG  
GACCTTGACAGTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGGTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC  
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTTGAATCTGCCTGGATGGAACCTGAG  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTTCATGCCTACACCCCCCTATTAAAGCAGAGTCTGGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRGTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQLRLHTAALPA

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**FIGURE 287**

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAGAATGGACTTGTAAATTGTCAT  
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA  
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC  
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC  
 TAAAGTTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG  
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC  
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA  
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG  
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTGTCTGTCTCCCAATCAGCTCAG  
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC  
 TAAATAGTGCTTTTCTCCAATGTGTCTCCAAGCAAGATTATCATTAACCTATAGGTTTCATGA  
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAATTGCAACACAAGATCAAT  
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT  
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCGTCT  
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA  
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT  
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTTACATCAGAGACTCTAGGT  
 GCTATATAATCCAAAACTTTTCAGCCTGTGCTCATTCTGTCCCATGCTGGCAATAATACC  
 TTGTGAGCCCATTACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT  
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC  
 TACCCCTTTTTTTGGAAGTTTCCAGCCGAATTTGAAATGAAATGACAAGGTGTATATTGTAT  
 CAATTTTTCATTCCCAACCATTCGATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT  
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT  
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTACATTT  
 TCGTATATTTATTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT  
 TGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGAAAAATTGCATACGTCTGTGCAATT  
 TTTTATCTGCCTAGTGCATTTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT  
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGGAAATGGGCTTTTGAAGCAACAATTTT  
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT  
 CCCACTTTGCAAACCTTTAACTACACATGCTTGGAATTAAGTTTGTAGCTGTTTTCATTGCTCA  
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQCK  
WSDEACRSSKRYICEFTIPK

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**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC  
CCCGAGCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAFLVGS AKPVAQPVAALSAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHIEGSQKCVAELGFPQAVGAVKALKALLGALTVEG

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**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC  
 CTTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCCTCCTG  
 GCACAGGTGTGGCTGGTACCCGGCTTGCCCCCAGTCCCTCAGTCGCCAGAGACCCAGGCCCC  
 TCAGAACCCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG  
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACCTTCGGATTACGCCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
 CAACATGGTCTTCTCCTCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGACTCAGAGAGACCCCTCTCCGCCAACCTGGAAC  
 GGGCCTCTCACAGGGGAGTTTGGCTTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCCATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGGAAAATTTCCAAAAT  
 GTTTGATGAGATTAATCCTGAAACCAATTAATTCCTTGTGGATTACATCTTGTTCAAAGGGA  
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC  
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAAGTTGCCTCCACCTTTGACAAGAA  
 TTTTCGTTGTCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
 TGGCTCAGAAACATGAAACCAGAAAACATGGAAGTTTCTTTCGGAAGTTCAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTACCCCTTGG  
 CTGACCTTAGTGAATCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC  
 TGCTTATTCATGCCTCCTGTCAATCAAGTGGACCGGCCATTTTCATTTCATGATCTATGAAG  
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAAT**TCAGG  
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAAGTATTAGGGTGTCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGATACATTCAAAGACCCCCAGCAGATGC  
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTCCTACATACATACCTATGAT  
 AAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACATAATAACAACATTAAGTAATA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTACAGTCTGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAGGGGAGATTTCA  
 CATCTCGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACAGAAATGGCATGC  
 TGCTTAAAGCTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTGGACCATGGT  
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATAAGGGAGGACTACTACAAA  
 GCATTAATTTGATACATATTTTAAAAA

**FIGURE 292**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L

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**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCG  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCCCTGGGCCGTGTCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCCAGTAGGGTCCAGGGGCCATCACTGCCCCGCCCTGTCCAAGGCCAGG  
CTGTTGGGACTGGGACCCTCCCTACCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA  
AAAAAAAAAAAAAAAA

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**FIGURE 294**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRLWVMPNHQVLLGPPEEDQDHIYHPQ

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**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG  
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGC  
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
 GACGCCCAGAAAAACGACATCTTATTACTCACCCATGAGCCAGCGGGAATTCAGTGGGGATT  
 GTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCAACGCCTTGTTGTGCTGGAATGAGGG  
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT  
 CCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATGTTGGTTA  
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG  
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA  
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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**FIGURE 296**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVFNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEGKCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHICIGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL  
FYR

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**FIGURE 297**

GCGGAGCGCGCGCGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
 CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGGACTCGGCGCGCGAGGTGCTTGGGCCG  
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAC  
 CACCAACTTCAGTTGCCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
 TAACCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT  
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTGTGGTGGTATTGTATTAAC  
 GCTGGGAGTTTTATCTATCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
 GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGGAAATCCATGGACCAAGGATGGA  
 ATACAGATTGATGCTGCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTCT  
 CTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT  
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT  
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
 TGCCATCTGGGCATACAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAACATCAACATTTTTTG  
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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**FIGURE 298**

MGLGARGAWAALLLGLTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH  
TNETSNSTVKPPTSVASDSSNTTVTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN  
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTGLVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII

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**FIGURE 299**

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCAGCCGGGAGCCGG  
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGCTGCGCCTTCCGTGCTGCTGCTGGC  
 GCAGCTGTGAGACGCCGCCAAGAATTTCGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT  
 CATGTTGTGGAGCCCATGCCTGTGCGGGGCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAATATGAAGAAAGAAGCTCTGTCAACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCATACTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
 TGCAAATGCACAGCATGTGCTAGCCCGCTCCCGAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCTCCTCAGC**TAA**TGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAGAAGCTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCCACCACT  
 GTTGCTGGAAGATTCAAAGCTGGAAGCAAACTTGCTTGATTTTTTTTCTTGTTAACGTA  
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG  
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTGAAGTCCTTTACCTGGAACA  
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAAGGTTTTTG  
 TTGTTGTTGTTTTTTGTTTTGTTTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT  
 AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATT  
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
 ACTTTTGCACGTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT  
 CTAAGATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCCTAGAACAAGCTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC  
 AGGGCTGGGGTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT  
 TCTTCCATATGCTCTTTTGAATGTAACAATAAAAAATAATTTTGAACATCAA

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**FIGURE 300**

MATLWGGLRLRGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS  
GHYIYNKNIS  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSVTIKVTIIIIYLSILGLLLLYM  
VYLT  
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLRASRSRANVLNKVEYAQQRWKLQVQEQ  
RKSVFDRHVVLs

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**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGCGTACTCCACAGTGCAGAGATCGCTCTGGCTT  
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCC GCGGGAAGCGG  
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA AAAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCA GTTTACATAAGAATG  
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTTGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPMMHHHQAPSDGQT  
PGARFQRSHLAEFAKAKSGGGAGGGGSGRGLMGQIPIYGFGLYILYILFKVSRILI  
ILHQ

09989734.111901

**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT  
 GGATTTGAAAGTTGAGAGCAGCATGTTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC  
 TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG  
 GGTGATTCAGCTCTGATGGGATGTGTTTTCCAGAGCAGAGAAGACAAATGTATATTCAAGAT  
 AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC GGTACACTTGATGGGGACATCTTATGC  
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAG  
 AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
 GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG  
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTTCCATCATG  
 CTTCAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
 GGTGTTCAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGACCTCGAACACTGGTGACCC  
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA  
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
 AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAGAAATCAGAGGCCACCTACATGACCATGCA  
 CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
 GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG  
 TGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTCAGACTCCCGCTCTC  
 CCAGCTGTCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCGTT  
 GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA  
 AAACCAACCCAAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSISGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDDGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV  
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNN SLEKKSGGGMPKTQQAF

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**FIGURE 305**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**  
GGATGAAGATGGATACATCACCTTAAATATTTAAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTGCGGCTGGTGGCTCTGGGGATTTGGTCTGTCTATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA  
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG  
AGAACAACATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

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**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEL  
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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**FIGURE 307**

CCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCGATCCGG  
CCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA  
GCCCCGGCAAACGCGAGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGCAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGCGGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCGAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGACAGCTGCAGGCGGATGGAACATTGATGGCACCAGGATGAGGACAGCACTTACACT  
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCAGCATCTCAGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC  
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCCTTACCCAAAAGTTCAAATTGTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498  
><subunit 1 of 1, 245 aa, 1 stop  
><MW: 27564, pI: 10.18, NX(S/T): 1  
MAAAIASSLRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRVSGVLNGGKSMHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153

096974.11901

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGCTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCCCT  
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTCTCTGACATTGGCAGTG  
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCTGTAGATTAC  
 AAGAGTGGATTGTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA  
 ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACTGGCTGCT  
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG  
 CGCGCTCCGGGCGCTGCCGTTTGGGGGTGTCTCTCCCGGGGCGCTATGCGGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCG  
 CGCAGCGGCGGTGTGTCCCCCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG  
 CTGTCCAAGTGCGACTGTGCGGGGGGCGGCCGCGCGGCGGACCGCGGCCCGGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTCTGTCGCCCGAGGGTTTCTACCTCCAGGCGAATCCCG  
 ACGGAAGCATCCAGGGCAGCCAGAGGATACAGCTCCTTACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTCTCTGCGCGGGC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGGAAACCGAGTTAAGAAGACAA  
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

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**FIGURE 310**

MAALASSLIRQKREVREPGSRFPVSAQRRVCPRGTKSLCQKQLLLLSKVRLCGGRPARPDR  
GPEPQLKGIIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPPSPAP

**Tyrosine kinase phosphorylation site:**

amino acids 199-207

**N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

**HBCF/FGF family signature:**

amino acids 131-155

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10511 126060

**FIGURE 311**

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGGAAATATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAAGTCAACAAGAGTAAGACAACATAG

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**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRRLR  
RQDPQLKGIVTRLYCRQGYLQMHPDGAIDGTDKDDSTNSTLFLNLPVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198

0999734-11901



**FIGURE 313**

GGGGAGGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTTTGGGTGCCCTTGCAAAAAAT  
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAATGTGTATATGTGCACACAGGAGCAITTCAGAAATG  
 AAATAAACAGAGTTAGACCCCGGGGGTGGTGTCTTGACATAAATAAATATCTTAAGCAGCTGTTCC  
 CTCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGATTCAAAAGAAAAAGTATGTTCAATT  
 TTCCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
 AGAACTGGTGGTGGTGGTGGTTCCTTTCTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAACATCTGC  
 AAAGAAATTCAGAGAAGAAAGTTGACCGGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCCAGCAGAGCA  
 CAGTTGGATTGTGCCATATGTTGACTAAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
 TTTTAAATTTTATTCCTTTGGTATCAAGATCATGGCTTTCTCTTGTCTTAACCACTGGATTTCCATCT  
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGACCAACCCAGATAAAATATGATGATG  
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTCTAGGTTTAAACAGGGCCCTATTGACCCCT  
 GCTTGTGGTCTGCTGCTCTTCAACTCTTGTGGTGGTGGTCTGCTGCGGGCTCAGACCTGCCCTTCTGTGT  
 GCTCTGCAGCAACAGTTGAGCAAGGTGATTTGTGTCGGAAGAACCTGCGTGAGGTTCCGAGTGCGATCTCC  
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAAACAGCTTCAAGCACTGAG  
 GCACTTGAATCCTACAGTTAGTAGGAACCATATCAGAACCATTGAATTTGGGGCTTCAATGGTCTGGCGA  
 ACCTCAACACTCTGGAACCTTTTGACAATCGCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAA  
 CTGAAGAGCTCTGCTGCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT  
 GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGCGCAACT  
 TGAGGTATTTGAACCTTGCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG  
 CTGGATCTTTCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTTCAGGCTTGTATGCACCTTCAAAAACT  
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGAGATCA  
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT  
 TTACATCACAAACCTTGAACCTGTAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAGCACTGGCCCCCTC  
 GAACACAGCTTGTGTGCCCCGGTGAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA  
 ATTACTTCATATGCTATGCTCCGGTGATTTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT  
 GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
 TGCGGCGTACAAAGTGCAGATAGCTGTGCTCAGTGAAGTACGTTAAATTTCAAAATGTAACCTGTGCAAGATA  
 CAGCGATGACACATGTATGCTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA  
 GCAACCACTACTCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCAAG  
 GACCAAGATAAACATGTGGGCTCCACTCCAGTGGTGCAGTGGGAGACCAACATGTGACCACCTCTCTCACAC  
 CACAGAGCACAAGGTGCAGAGAGAAAACCTTACCATTCCAGTGACTGATATAACAGTGGGATCCAGGAAT  
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGGTGTTTGTGGCCATCACATCATGGCTGCAAGTATGCT  
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA  
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGGCCCTGCCATGCCTGCTATCGAGCATGAG  
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACACAGTTAAACACAATAAATCAATACA  
 CAGTTCACTGATGAACCGTTATTGATCCGATGAACCTCAAGACAATGTACAGAGACTCAAACTCTAAACAA  
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGCTTTATTAATAATGACACAATGACTGGGCTAA  
 ATCTACTGTTTCAAAAAAGTGTCTTTCAAAAAAACAAGAAAGAAATTTATTTATTAATAATTTCTATTG  
 TGATCTAAAGCAGACAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNALFDPILLVLLALQLLVVAGLVRAQTCPSVSCSNQFSKVIC  
 VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS  
 YISEGAFEGLSNRLYNLAMLNREIPNLTPLIKLELDLSGNHLAISIRPGSFQGLMHLQKL  
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVNSVGN  
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ  
 STRSTEKFTTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
 HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS  
 VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
 434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
 391-397, 422-428, 433-439, 531-537

**FIGURE 315**

GCGCGGGGAGCCCATCTGCCCCAGGGGACGGGGCGGGGCGGCTCCCGCCCGGCACAT  
 GGCTGCGAGCCACCTCGCGCGCACCAGGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
 GCGCGCCCGGCGCGCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCGCGTCCGGGGATC  
 GGGATGTCCTCCTCCTCTCTCTCTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCTGCCACCATCACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGCAGTGAGTGCATCCTTGGCAGAGAGCCATTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAAGTGTACAGT  
 ATGTACAAGACATCCGATGGTGTGAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAGCCCTTCTGTGAACCCAGCT  
 CCTTCTTCAGGCTCTCGGAGCTCAGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT  
 AGTGCCTCAGCGACCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG  
 CTAATCTGACCAAGCAGAAACCACACCAGCATGATCCCAGCCAGAGCAGACCTTCCAA  
 ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGACCGGAACAGATTAGATGAGCATTTTCTTATACAATACCAACAAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTGTGTGACAGGACCTGTGGTGAGAAGGTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT  
 ATTAGTTATTCAGACAGTCAAGCAGAAACCACAGCCTTATTACCTGTCTACACCATGTAC  
 TGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTGCTCTTCTATTCTGACTTAAC  
 TTCAATTTGTCTAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTTGACAAAGGATTGTGAAGAGCTTTCATCTTCATGATGTT  
 ATGAGGATTTGTGACAAACATTAGAATATATAATGGAGCAATTGTGGATTTCCTTCAAT  
 CAGATGGCTCTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAAAACACATGTCAATT  
 TATCAAGCTCTCTAGAAAGAATTTCTCTAGAAAAAAGGGATCTAGGAATGCTGAAAGATTA  
 CCAACATACCATTATAGTCTCTCTTTCTGAGAAAAATGTGAACAGGATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGCACTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

00000734.11601

**FIGURE 317**

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGGAGGCCGCCTACCTGCAGCGCCGCGCCACGGGCACGGCAGCCA  
 CCTATGCGCGCTCTGCTGTGCTTCTGTGCTCCTGTGCGGAGTAGTGGATTTCGCGCAGAAGTTTGAGTATCACTACT  
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCTCCCGAAGA  
 CACGGGACCGCTGGACATCTGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT  
 ATCTGCGAGACAATAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC  
 AAAATCTGGTGATGCATCAATTAATATACGAATTTACAACTGTGCAGATATTGGCAGCATATCAGTGCAAAAGTAA  
 AAAAGCTCTGCTGTCTGTCAATAAGAAGATTATCATCTGGTAGTCTCTGTTAAGCCTTCAGGTGCGAGATGTTACG  
 TTGATGGATCTGAAGAAATTCGAAGTGACTTTAAGTAAATGTGAACCAAGAGAGGTTCACTTCCATTACAG  
 TATGAGTGGCAAAATTTGCTGACTCAGAAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT  
 ATCTGTAATAAATGCTCTCTGACTACTCTGGGACATACAGCTGTACACTCAGAAAACAGAGTGGGCTCTGATC  
 AGTGCTCTGTGGCTCTAAAGCTGTCCCTCCTTCAAAATAAGCTGAGCAATTTGACGAGGCCATTATAGGAAT  
 TTGCTTGTCTAGCGCTCATTGGTCTTATCATCTTTTGTCTGCTGTAATAAGGCCGAGAGAGAAAAATAGAAA  
 GGAAGTTATCATCAGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCACCTGCCAGAGCTACATCG  
 GCAGTAATCATTATCCTCGGGCTCCATGTCTCCTTCCAACATGGAAGGATATCCAAAGACTCAGTATAACCAA  
 GTACCAAGTGAAGACTTTGAACGCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAGTACCCTTACAA  
 GACTGATGGAATTACAGTTGTATTAATAATATGGACTACTGAAGAATCTGAAGTATTGATTATTTGACTTTATTTT  
 AGGCCTCTAGTAAAGACTTTAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGCAGCTGTAAGAACAC  
 ATCTACTTTATGCAATGGCATTTAGACATGAAGTCAGATGTCATGTCAAATTAGTACGAGGCCAATTCCTTGT  
 TAAAAAACCTATGTATAGTACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCCTAACAA  
 ATTTTAACTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGATGGTTAAATAGTTGATTTTCAA  
 AGGAAATTTTAAATCTTACGTTCTGTTAATGTTTTTGTATTTAGTTAAATACATTGAAGGGAAATACCCG  
 TCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTATGCGCTCAAACATTTTTTTATTTGCAACTACA  
 TGATTTACACAATTTCTCTAAACACAGACATAAATAGATTTCTGTATATAAATAACTTACATACGCTCCA  
 TAAAGTAAATTTCTCAAGGTGCTAGAACAATCGTCCAGTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC  
 ACAATATATAAATACTCAAGTCCCAATTTAAACCTTAGGCACCTTGACTAATTTTAAATAAATTTCTCAAAC  
 TATCAATATCTAAAGTGCATATATTTTAAAGAAAGATTATCTCAATAACTTCTATAAATAAAGTTTATGAG  
 TTTGCGCCATCTAAGTCTACTATATTAGTAAAGCTTTTAACTTTTAAATGTTGATAGTAAAGTTTATCTACCTT  
 TTTCTCAACATGAACCCAAACACAAATCAAACGAACTTAGTGAGTGCTAAACATGTGAGGATTATCCAGTGAT  
 TCCGCTCACAATGCATTCAGGAGGAGGTACCCATGTCACTGGAAATGGGCGATATGGTTATTTTCTTCTCC  
 TGATTTGGATAACCAATGAACAGGAGGAGGATAGTGATTTGATGGCCATTCCCTCGATACATTCTCTGGCTT  
 TTTTCTGGGCAAGGCTGCCACATTTGAAGAGGTGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT  
 TAAGTTAATTCAAGGAAAAAATCATCATCTATGTTCCAGATTCTCATTTAAGACAAAGTTACCCACAACAT  
 GAGATCATCTAAGTGACACTCTTATGTCAGTCTAAATACATTAACAACTCATGTGTAATAGGCGGTATAA  
 TGTATAACAGTGCACCAATGTTTCTGATATGCATAAAGAAATGAATAAATCAACACAGTACTTCTTAAACAA  
 CTTCAACCAAAAAAGACCAAAAGCTGAACGAATGAAGCTTTGAAGACATGCTGTTTATGTTCCGATGGGTT  
 CCACAGCTGGCTAGCCAGGAGTCACTTGGAGGCTTTTAAATCAAAACATTTGAGCTGGAGGCGATTATCTCTT  
 AGCAAACTAATGCAGAAAGCAAAAATCACTACCGCATGTTCTCACTTATAGTGGGAGTAAATGATGAAGACT  
 TATGAACACAAGAGGAGAAACATAGACATTTGGAGTCTATTGAGAGGGAGGTTGGAGAGGAAAGAGGCA  
 GAAAGATTAACATTAGATGCTGCTTACACCTGGGTGATGAAATATATGTACAACAAATCCCTGTGCACCA  
 GTTTTACCTATGGAACAAACCTTCACTGTATCCCTAAACCTAAAAATAAAGTTTAAAAAAAATAAAGAAAA  
 AAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAA  
 AAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAAAATAAAGAAAA

0980734-11501

**FIGURE 318**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
```

&gt;&lt;subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGFLDIEWLISPA  
DNQKVDQVILIYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNTNLQLSDIGTYQCKVKK  
APGVANKKIHLVLVLPKPSGARCYVDGSEEIGSDFKICEPEKESLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVNRVRNGDQCLLRNLRVVPPSNKAGLIAIAIGTLL  
ALALIGLIIFCCKRKRREEKYEVHHDIRVEDVPPKSTARSYSIGSNHSLSGMSPSPMN  
EGYKSTQYNQVPSDEFTKQPSPTLPAPKFYPKYTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGTGCCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC  
 C'CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC  
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGCACACAGGCGGTTTTCTGTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC  
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA  
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT  
 TTGGCCAGGATTATGTCAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCCTCTGGATGCTGTGAAGAGCTACAGAGAAGATTCTTGTAATTTATTACAACCTATTTT  
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTAAAAAACAGAGAGGGATGCTTGATGTAAAACTGAACCTCAGAGCATGAAAAACACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCAAT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0989734.11301

**FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFFCPPLLATASQMVMVVLPCLGFTLLLSQVSGAQGEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

09989734.11901



**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGCTGTATTTT  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTC AAGGATCA  
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

00000000.11000

**FIGURE 322**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRLCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETLIQIKPLDVCVTKNLLAFYVDVRFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
ROCHCRQEATNATRVIHNDNYDQLEVHAAATKSLGELDVFLAWINKNHEVMFSA
```

**Signal sequence:**

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACATGCACCTC  
GGTICTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGC**ATG**TTGGGGGCCGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTTGGATCACACTATTTGAC  
CCGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCTCC  
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCAAGAGAGCCTTCTGCCAGGCATGAACC  
CACCCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC  
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCG  
CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLTYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY  
DVIHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE  
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA  
KFI

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

09989734.11001

**FIGURE 325**

GGAAGAGGTACCCGCGAGAGACGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTCTTCTTCTGTGGGAGGTTGGGGTCTCTGG  
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
 ACCTCTTCTAGGGCTCAACCCGAGCGGCCCATTTCCAGAAGCAGAGACCAGGGGAGCCAA  
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGC  
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA  
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC  
 ACCCGTTCAGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC  
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCTAT  
 GGTCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG  
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCTCAGA  
 CATAGATCTCATCCCCACGAAGGGGTGAAGGCTCGTCCACCTCCGATCCACCAGCTCTGC  
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTCC  
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA  
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA  
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC  
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCCGGAAGCCGCCCTCAAGAACTTCACCC  
 CTTTCAGAGACACCACCATTGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCT  
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC  
 GAGGCCGACCACAGAG**TGA**GTGCAGGTGAAATGGAGTTTCTCTCTCTGCGGCTGAGTG  
 TGGCTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
 CGGGAATCCAGGCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTGAGAGAGGCTA  
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGCTGTGCCCTAGCCTG  
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
 AAGGGCAGCATGTCCAAGCCCCAACCCAGATGTGGCAACAGGACCCCTCGCTCACATCCAC  
 CGGAGTGATGTATGGGGAGGGGCTTACCTGTTCAGAGAGGTGTCCTTGGACTCACCTTGG  
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
 TTAAATTAACCTCAGTGTGGCCCAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA  
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM  
 TTVQQTITGSDPEEAI FDTLCTDDSSEEAKLTMDILT LAHTSTEAKGLSSESSASSDGPHPV  
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTL LAEALVTVTNI  
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAE TL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALS VETPSY  
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYPSEAA LKNFTPSETPTMDIATKGPFPTS RD  
 PLPSVPPTTTNSSRGNTSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

09989734.11901

**FIGURE 327**

GCGGAGCATCCGCTCGGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCGCGG  
 GCGGACAGAGCTGTCTCGACCTGGATGGCAGCAGGGGCGCGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCTCTGTGACGCTTCTTAAAGCAAATAGACCAGAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAAAT  
 GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGCCATTGAACACGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC  
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAGGCCATTCTCAGAGTTTCACAATTTTCTCTGATCAAGAAA  
 TAGTCTCATCTGCTGCCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCATGTCACCTTCTC  
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGGAGTGTTCAGAAAATCAGTACGGCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAAATCCTTTGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCATT  
 TAGTAACAGAGCCCAAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCAGAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG  
 GTCTCAAACTCCTGACCTAGTGATCCACCTCCTCGGCTCCCAAAGTGTCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAAGT  
 GGAACCAAATTAGTAATTTTGGGTAATCTGTCTCTAAATATAGCTAAACAAAGCTCT  
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCAGATAAAATCAAC  
 TGTTTATCAAAATTTCTAATGAGTTGCTTTCTTTTATATGGATTCTCTTTAAACTTAT  
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

0999734-111901

**FIGURE 328**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
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><subunit 1 of 1, 431 aa, 1 stop
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><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGEGESLTYTLVITVICFLTRLRLSASQNCCLKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMI FDRKTRARQPNCLYFFCNEEACPLKPAKGLMSYRIITDF  
SLTRNLPSELPEQEDSLHLGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFSSDHLLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHLLENVVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSGQPLATAPPVNTTVTSGPPTTLISVFTRAAATLQAMATAVLTTLTFAQ  
TDKSGSLTIFTEIENLTNLNTGVNVTALSMSNVSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEKWLIGSLFGVLVFLVIGVLGRLISESLRRKRYSRLDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321



CTCCACGGTGTCCAGGCGCCAGAAATGCGGCTCTGGTCTGCTATGGGTTGGCTGTGCTGCTCCAGGTTATGAACCTCTGGAGGGCCAGAGGAATACGGGGTTCGAAGGGGACATGCTGTGCCGTGCAGTCCAGCTACAGGAAGAGTGTAGGACACCGGAAGTCTGGTCAGGAAGGTTGGGATCCTCTTCTCTGCTGCTCTGCACCACTTATGCAAGAAAGAACGCCAGGAGACAATGAAGGCGAGGTTGACGTCCTCCGTGCAGCGCCAGGAGCTCTCGCTCATTTGTACCTTGTTGAACCTCACCTCGAAGCAGCTGGGGAGTATGGTGTGGGTCGAAAAACGGGGCCCGATGAGTCTTTAGCTGATCTCTGTTGCTCTTTACAGGACCTGTCTCTCTCCCTCCCTCTCCACCTCTCCAGGCTCTGGCTACAACACGCTGCAGCCAGGCAAAAGCTCAGAAAACCCAGCCCGAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCAGCCAAGCAGGGGAAGACAGGGCGTGAAGGCCCCCTCCATTTGCCAGGAGACTTCCGATACGGGCAGGAAGGACTTCTCATGACAGGAAGTAATCTCACCAGGAGACTCTCTCTCTGTCAGGAGGACTCCCGCCCCCATCGACGTGGACTCCACCTCAGCAGAGGACACCACTGTACAGCTTCTCAGCATGGCAGCTCTAAGCCGAGGTGTCTCCATCCCGATGGTCCGATACCTGCCCAGTCTGGTGGTCTGAGCCTTCTGTGACGCGAGGCTGATCGCTTTGCGAGCCACTGTCTCTGTGAGAAAGTAAGCTCAACAGGCCACGGAAGAGAGAGGAACTCTGAGGGGACGTGATCTCGATGCTCTCCCTCCACATCTGAGGAGAGCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGTGAACGAGTATGGCTGGCTGGATCAGCACCGGATCCCGAAAGCTTTCCACCTCAGGCTCAGAGTCTCAGCTGCCGAGCTCAGGCGCTCTCCACCGCTCTCCACCGCTCTCTCTGTGATGCTTGTGATTTGCCAGCTGACCTTGAAGAGCTTTGTCTCAGCCCTGGAGCCGAGAGCGGTGGCTGCTTGTCTCCGGTCTGAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAAGTACCAGCTGTGACCTGACGAGGCCACAGCAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGCTCATGCCCCAGTGTGGAGCCTCTCTCTCTCCCACTCAGACCCCACTTGTCTTCCCTCCCTGGCGTCTCAGAGTTAGCTCCACGGTCTCTGTCATCAGCTGGTGATGAAGAGGAGCATGCTGGGCTGAGACTGGGATTCTGCTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAACGCTGATTTCTGGGCCACAGAACCCACAAAACCATCTCTGGGCTTGGTGCGAGGACTCTGAATTTCAACAATGCCAGTGACTGTGCATCTGAGTTTGAGGCCAGTGGGCGCTATGAAGCTCACCTCTCAGCTTCAGCTTGTGCTGATGCTGAGCTCTCCACTGCCCTCCCAATGATCTGCTGTCTGTCGACACAGATGACAGTGGGACTCCCTGAGGCTCTGTAAGTCCAGGCCCTGGTTCAGGTTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGGTTGGCTTTTNCATTTTGGCTCTCTGGNCCATGCCTCTTGGCTTTGGAAGAAATGATGAGAAGAACTTGGCTCTCTTGTGTCGAAAGGTTACTTGCTATGGGTTCTGGTGCTAGAGAAGAAAGTAGAAAACAGAGATGCACGTAGTGTCTAACACAGAGGAGATAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCAGGCCCTCGAGAGGGGTGGGGGTGGTGGTAAGTAGCAACACTACTATTTTTTTCTTTTCCATATATATGTTTTTAAAGCAGAATCTCGTGCTGTGCCACAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCGCCCTCTGGGTTCAAGTGATTTCTTGCTCTCAGCTCCCGAGTAGCTGGGATTACAGGCACGACCAACCACTGGCTAAATTTTGTACTTTTAGTAGAGATGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAAATGAGCCTCTGCTCTCAGCTCCCAAATTCGCGGATTCACAGGATGAGCCACTGTGTCGTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTTCAGTATGCAAAACTTGAAGAAATGAGGAGAAAAAGGAAGGAAAAAATGTACCCATAGCTCTCACCAGAGCAATATCATTTCTGTTGTTGTACTTCTTCCACTCTTTTCTCTTCACATAATTTGCGGTGTTCTTTTACAGAGCAATTATCTTTGATATACAACTTGTATCTGTGCTTTTCCACTTATCGTTCCATCATTTTATTTCCAGCACTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCATGTGCATATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCVGVEKRGPD E SLLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG  
TSQYGHERTSQYTGTSPPHATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE E KEAPSQAPEGD  
VISMPPLHTSEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128